



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 104187

To: Terra Gibbs
Location: CM1-11E12
Art Unit: 1635
Tuesday, September 23, 2003

Case Serial Number: 09/840704

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 09-23-03
Searcher: Beverly C 4999
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
☒ Other CEJ

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STIC-Biotech/ChemLib

104187

From: Gibbs, Terra
Sent: Wednesday, September 17, 2003 6:11 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

RECEIVED

SEP 22 2003

Please search SEQ ID NO:1 of USSN 09/840,704.

TECH/BIOL DIVISION
10/10/

Please do a search in all commercial databases.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
CM1, 12A12
703-306-3221

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
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AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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AR182654
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VERSION
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SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

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Sequence 1 from patent US 6338958.
AR182654.1 GI:20225861
Unknown.
Unclassified.
1 (bases 1 to 1789)
Dedhar S. and Hannigan, G.
Integrin-linked kinase and its uses
Patent: US 6338958-A 1 15-JAN-2002;
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DEFINITION Sequence 3 from patent US 6177273
ACCESSION AR125502
VERSION AR125502.1 GI:14111564
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Bennett, C. Frank, and Cowser, L. M.
TITLE Antisense modulation of integrin-linked kinase expression
JOURNAL Patent: US 6177273-A 3 23-JAN-2001;
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE Hannigan, G.E., Leung-Hogesteejn, C., Fitz-Gibbon, L., Coppolino, M.G.,
 Radeva, G., Filmus, D., Bell, J.C. and Dedhar, S.
 Regulation of cell adhesion and anchorage-dependent growth by a new
 beta 1-integrin-linked protein kinase
 Nature 379 (6560), 91-96 (1996)
 JOURNAL MEDLINE 96135142
 PUBMED 8538749

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REFERENCE 2 (bases 1 to 1789)
AUTHORS Dedhar, S. and Hannigan, G.E.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1995) Shoukat Dedhar, Cancer Biology Research,
Sunnybrook Health Science Centre and University of Toronto, 2075
Bayview Avenue, North York, Ont. M4N 3M5, Canada
REFERENCE 3 (bases 1 to 1789)
AUTHORS Dedhar, S. and Hannigan, G.E.
JOURNAL Direct Submission
TITLE Submitted (21-MAY-1998) Shoukat Dedhar, Cancer Biology Research,
Sunnybrook Health Science Centre and University of Toronto, 2075
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REMARK Sequence update by submitter
COMMENT On May 21, 1998 this sequence version replaced gi:2648173.
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LOCUS AR270508 1786 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1071 from patent US 6500938.
ACCESSION AR270508
VERSION AR270508.1 GI:29701742
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1786)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1071 31-DEC-2002;
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source 1..1786
location/Qualifiers
BASE COUNT 443 a 486 c 479 g 378 t
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Query Match 99.0%; Score 1771.4; DB 6; Length 1786;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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RESULT 8
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LOCUS AX524966
DEFINITION Sequence 13 from Patent EP1236799.
ACCESSION AX524966
VERSION AX524966.1 GI:25170048
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Specht,T., Hinzmann,B., Schmitz,A., Pilarsky,C., Dahl,E. and
Rosenthal,A.
TITLE Human nucleic acid sequences derived from breast tumor tissue
JOURNAL Patent: EP 1236799-A 13 04-SEP-2002;
metagen Pharmaceuticals GmbH (DE)
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Query Match 94.7%; Score 1693.4; DB 6; Length 1780;
Best Local Similarity 99.1%; Pred.No. 0;
Matches 1745; Conservative 0; Mismatches 11; Indels 5; Gaps 4;
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LOCUS Human nucleic acid sequence originating in mammary tumor tissue.
DEFINITION BD134433
ACCESSION BD134433.1 GI:23229378
VERSION JP 2002506643-A/11.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1780)
AUTHORS Speft T., Hintzman, B., Armin, S., Pitarski, C., Edgar, D. and Rosenthal, A.
TITLE Human nucleic acid sequence originating in mammary tumor tissue
JOURNAL Patent: JP 2002506643-A 11 05-MAR-2002;
COMMENT METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002506643-A/11
PD 05-MAR-2002
PF 19-MAR-1999 JP 2000536852
PR 20-MAR-1998 DE 198 13 839.3
PI THOMAS SPEFT, BERND HINTZMAN, SHOWITT ARMIN, CHRISTIAN PIRARSKI, PI DUHL EDGAR.
PI ANDRE ROSENTHAL
PC C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61P35/00, C07K14/47, C07K16/18,
PC C12N1/19, C12N5/10, C12N15/00, A61K37/02, C12N5/00 CC Human
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BASE COUNT 427 a 489 c 492 g 372 t
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Query Match 94.7%; Score 1693.4; DB 6; Length 1780;

Best Local Similarity 99.1%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 11; Indels 5; Gaps 4;
QY 24 ACGGAGGTTCCTCCCGAGAGAGGATCCTGCAGCCCGAGTCCCGAGGATAAAGCTTGGGGTTC 83
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LOCUS	BC001554
DEFINITION	BC001554 Homo sapiens integrin-linked kinase, mRNA (CDNA clone MGC:5051 IMAGE:3457801), complete cds.
ACCESSION	BC001554
VERSION	BC001554.1 GI:16306740
KEYWORDS	MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1731)
AUTHORS	Straubner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klusener,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Butow,K.H., Scheeler,C.F., Bat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schaefer,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.U., Bosak,S.A., McPwan,P.J.,

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CDS	<p>452 a 464 c 458 g 357 t</p>
BASE COUNT	452 a 464 c 458 g 357 t
ORIGIN	92.4% Score 1652.6; DB 9; Length 1731;
Query Match	

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Matches 1678; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

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RESULT 11
MMU94479

LOCUS MMU94479 1750 bp mRNA linear ROD 02-JAN-1998

DEFINITION Mus musculus integrin binding protein kinase mRNA, complete cds.

ACCESSION U94479

VERSION U94479.1 GI:2739449

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1. (bases 1 to 1750)
Li, F., Liu, J., Wayne, R. and Wu, C.
Identification and characterization of a mouse protein kinase that
is highly homologous to human integrin-linked kinase
Biochim. Biophys. Acta 1358 (3), 215-220 (1997)

JOURNAL 98031580

MEDLINE 9366252

PUBMED 9366252

REFERENCE 2. (bases 1 to 1750)
Wu, C. and Li, F.
Direct Submission
AUTHORS

TITLE

JOURNAL

FEATURES

source 1. 1750


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BC003737      1673 bp      mRNA      linear      ROD 16-APR-2003
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DEFINITION    IMAGE:3601214), complete cds.
ACCESSION     BC003737
VERSION       BC003737.1 GI:13277656
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SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1673)
Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerker,A., Schein,J.E., Jones,S.J., and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1673)
Straussberg,R.
Direct Submission
Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdopaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 11 Row: d Column: 18
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 Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 REFERENCE 1 (bases 1 to 1693)
 AUTHORS Ishii, T., Satoh, E. and Nishimura, M.
 TITLE Integrin-linked kinase controls neurite outgrowth in NIE-115 neuroblastoma cells
 JOURNAL J. Biol. Chem. 276 (46), 42994-43003 (2001)
 MEDLINE 21560993
 PUBMED 11560928
 REFERENCE 2 (bases 1 to 1693)
 AUTHORS Ishii, T.
 TITLE Direct Submission
 JOURNAL Submitted (15-Apr-2000) Veterinary Pharmacology, University of Obihiro, School of Veterinary Medicine, Nishi 2-Sen 11, Inada-Chou, Obihiro, Hokkaido 080-8555, Japan
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RESULT 14
AC132877

LOCUS
DEFINITION AC132877 192539 bp DNA linear HTG 12-MAR-2003
Mus musculus clone RP24-216J21, WORKING DRAFT SEQUENCE, 7 unordered
pieces.

ACCESSION

AC132877.3 GI:28927732

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Birren,B., Nussbaum,C. and Lander,E.
1 (bases 1 to 192539)
Mus musculus, clone RP24-216J21
Unpublished

REFERENCE

2 (bases 1 to 192539)

AUTHORS

Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 192539)

AUTHORS

Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Faro,S.,
Diaz,J.S., Dodge,S., Doolley,K., Dorris,L., Erickson,J., Fero,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2003 this sequence version replaced g1:28412043.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: W1BR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L27122

Center clone name: 216-J21

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.96071

Consensus quality: 19104 bases at least Q40

Consensus quality: 191385 bases at least Q30

Consensus quality: 191502 bases at least Q20

Insert size: 191939; sum-of-coverage

Quality coverage: 9.6 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 7935: contig of 7935 bp in length
* 7936 8035: gap of 100 bp
* 8036 10717: contig of 2682 bp in length
* 10718 10817: gap of 100 bp
* 10818 21133: contig of 10316 bp in length
* 21134 21233: gap of 100 bp
* 21234 37038: contig of 15805 bp in length
* 37039 37138: gap of 100 bp
* 37139 73158: contig of 36020 bp in length
* 73159 73258: gap of 100 bp
* 73259 134748: contig of 61490 bp in length
* 134749 134848: gap of 100 bp
* 134849 192539: contig of 57691 bp in length.

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Location/Qualifiers

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/db_xref="taxon:10090"

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73259..134748

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134849..192539

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Best Local Similarity 86.2%; Pred. No. 0; Indels 22; Gaps 6;
Matches 1452; Conservative 0; Mismatches 211

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QY	882	CAGATTTTTCGCATCCAAATGCTCTCCAGTGTAGTGTCCAGTCTCCACCTGC	941
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D 101463 GAAGAGCCTGAAGACACAAACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGCCTTCT 101522
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D 101523 GTGGAACTGTGTACACAGAGAGGTGCTCTTTGTGACCTCTCTAATATGAATATGGAAAT 101582
QY 1362 GAAGTGGCATTTGGAAGCCCTTCGCGCTPACCATCCCAACAGGATTTTCCCTCATGTGTG 1421
D 101583 GAAGTGGCATTTGGAAGCCCTTCGCGCTPACCATCCCAACAGGATTTTCCCTCATGTGTG 101642
QY 1422 TAAGTCTATGAATCTGCATGAATGAAGACCTTGCAGAGCGACCCCAATTTTGACATGAT 1481
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QY 1482 TGTGCTATCTCTGAGAAAGATGACAGCAAGTAGGACTGGAAGGTCTTGCCTGCACTCC 1541
D 101703 TGTGCTATCTTGGAGAGATGACAGCAAGTAGGACTGGAAGGTCTTGCCTGCACTCC 101762
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pieces.
AC093480
VERSION AC093480.2 GI:22325292
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 209228)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-61L24
Unpublished
2 (bases 1 to 209228)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cook,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

```

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Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Olive,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,K., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembeke,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (26-AUG-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 209228)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Fato,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembeke,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 20, 2002 this sequence version replaced gi:15290930.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L14395
Center clone name: 61_L24
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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Consensus quality: 208763 bases at least Q30
Consensus quality: 208883 bases at least Q20
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Insert size: 208928; sum-of-ctnigs
Quality coverage: 14.5 in Q20 bases; agarose-efp
Quality coverage: 15.3 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 13553: contig of 13553 bp in length

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TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2003, 15:19:24 ; Search time 369 Seconds
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13087.519 Million cell updates/sec

Title: US-09-840-704a-1

Perfect score: 1789

Sequence: 1 gaattcattctgcgcgcct.....aaaaaaaaaaaaaaaaaaaa 1789

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues 5105512

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
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- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1787.4	99.9	1789	22	AAf69274
2	1787.4	99.9	1789	24	ABK84315
3	1773	99.1	1786	18	AAf71716
4	1771.4	99.0	1786	25	ACA56473
5	1693.4	94.7	1780	20	AA233623
6	1352.6	75.6	1607	21	AAf18317
7	1195.8	66.8	1359	22	AAf90197
8	466.8	26.1	1820	23	ABL15659

c	9	451.2	25.2	567	22	AAH09626	Human cDNA clone (
c	10	328.4	18.4	330	21	AAf78148	cDNA encoding huma
c	11	328.4	18.4	330	22	AAf18886	Colon tumour relat
c	12	328.4	18.4	330	25	AB233072	Human colon tumour
c	13	305	17.0	4354	23	ABL16568	Drosophila melanog
c	14	240.8	13.5	568	25	AAH35546	Human colon cancer
c	15	228.8	12.8	285	25	ABX74732	Human cDNA sequenc
c	16	133.8	7.5	152	19	AAV33551	Clone 18416 cDNA
c	17	127.8	7.1	301	24	ABK62280	Rat sequence diffe
c	18	90.2	5.0	508	22	AAH04110	Human cDNA clone (
c	19	84.8	4.7	6843	25	ABX34513	Human mdct cDNA SE
c	20	84.8	4.7	7185	22	AAH57380	Human skeletal mus
c	21	75.6	4.2	2355	24	ABA90356	Human polynucleoti
c	22	75.6	4.2	2355	25	AB224424	Human death associ
c	23	75.6	4.2	3981	24	AB212023	Human polynucleoti
c	24	75.4	4.2	896	22	AA333235	DNA encoding human
c	25	75.4	4.2	1640	24	ABN85315	Human cytoskeleton
c	26	75.4	4.2	1783	22	AAf16004	Human polynucleoti
c	27	75.4	4.2	2894	22	AAf58218	Human polynucleoti
c	28	75.4	4.2	4935	25	AAH51581	Human structural a
c	29	75	4.2	977	22	AA333358	DNA encoding human
c	30	73.4	4.1	696	20	AA335854	DNA encoding rat g
c	31	72.4	4.0	2499	22	AA306739	Polynucleotide seq
c	32	71.2	4.0	1288	21	AAZ49052	Human ankyrin fami
c	33	71.2	4.0	1345	21	AAZ94868	Human MHC class II
c	34	70.8	4.0	3876	22	AAH15762	Human cDNA sequenc
c	35	67.6	3.8	3517	23	ABL10131	Drosophila melanog
c	36	67	3.7	621	22	AAK52295	Human polynucleoti
c	37	67	3.7	678	18	AAf66424	Human P28 coding s
c	38	67	3.7	780	20	AA335852	DNA encoding human
c	39	66.4	3.7	1468	18	AAf66425	Human P28 coding s
c	40	66.4	3.7	5482	22	AAf63955	Human P28 coding s
c	41	66.4	3.7	5484	23	ABL08154	Drosophila melanog
c	42	66.4	3.7	10194	23	ABL08154	Drosophila melanog
c	43	65.4	3.7	696	20	AA335853	DNA encoding mouse
c	44	65.4	3.7	1534	25	AAH49614	Human cytoskeleton
c	45	64.8	3.6	3779	25	ABX34495	Human mdct cDNA SE

ALIGNMENTS

RESULT 1
ID AAF69274 standard; DNA, 1789 BP.
XX AAF69274;
AC AAF69274;
XX
DT 18-APR-2001 (first entry)
XX
DE Human integrin-linked kinase DNA.
XX Antisense; integrin-linked kinase; hIK; infection; tumour;
KW Inflammation; ds.
XX
OS Homo sapiens.
XX
PN US6177273-B1.
XX
PD 23-JAN-2001.
XX
PF 26-OCT-1999; 99US-0428219.
XX
PR 26-OCT-1999; 99US-0428219.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsett LM;
XX WPI; 2001-137069/14.
DR
PT Novel antisense compounds capable of modulating expression of human
Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment

XX 14-AUG-2002 (first entry)
XX
XX Human cDNA differentially expressed in granulocytic cells #886.
DE
XX
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW fungal infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
OS
XX Homo sapiens.
XX
XX MO200228999-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US30821.
XX
XX 03-OCT-2000; 2000US-237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
PT of gene associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX Claim 1; SEQ ID No 886; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published/pct_sequences.

XX	Sequence	1789 BP: 443 A; 488 C; 480 G; 378 T; 0 other;
SQ		
	Query Match	99.9%; Score 1787.4; DB 24; Length 1789;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 1788; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GAATTCATCTGTGACATGCTACACACGGAGTTCCCGGAGAGAGATCTCTGACCCGAGT	60
DB	1 GAATTCATCTGTGACATGCTACACACGGAGATTCCCCGAGAGAGATCTCTGACCCGAGT	60
QY	61 CCCGAGATTAAGTTGGGTTTCATCTCTCTCTCTGATCATCTCCACAGTCCCTCAGCT	120
DB	61 CCCGAGATTAAGTTGGGTTTCATCTCTCTCTCTGATCATCTCCACAGTCCCTCAGCT	120
QY	121 TCCCAATCCAGGGGACCTCGGCGCGGGGACGCTCTATGACGACATTTTTCACATGAC	180
DB	121 TCCCAATCCAGGGGACCTCGGCGCGGGGACGCTCTATGACGACATTTTTCACATGAC	180
QY	181 CGGAGGGGCAACGGAGTGGCCGTTGCGCTGTGGTGACCAACGAGAGAAAGCATCTCAAC	240
DB	181 CGGAGGGGCAACGGAGTGGCCGTTGCGCTGTGGTGACCAACGAGAGAAAGCATCTCAAC	240
QY	241 CAGGGGGACCATCATGGCTTTCCCCCTTGCATCTGGGCTTCGCCAGAGGGCCGCTTCGT	300
DB	241 CAGGGGGACCATCATGGCTTTCCCCCTTGCATCTGGGCTTCGCCAGAGGGCCGCTTCGT	300
QY	301 GTGGTTGAGATGTTGATCATGCTGGGGGGCAACGATCAATGTAATGAACCGTGGGGATGAC	360
DB	301 GTGGTTGAGATGTTGATCATGCTGGGGGGCAACGATCAATGTAATGAACCGTGGGGATGAC	360
QY	361 ACCCCCTGTCATCTGGCAGCCAGTCATGACACCCGTGATATTGACAGAACTATTGACAG	420
DB	361 ACCCCCTGTCATCTGGCAGCCAGTCATGACACCCGTGATATTGACAGAACTATTGACAG	420
QY	421 TACAAAGGCAATCATATGACAGTAAATGAACACGGGAATGTGCCCTGCACTATGCTGT	480
DB	421 TACAAAGGCAATCATATGACAGTAAATGAACACGGGAATGTGCCCTGCACTATGCTGT	480
QY	481 TTTTGGGGGCCAAGATCAAGTGGGACAGAGACCTGGTGGCAAAATGGGGCCCTTGTGACATC	540
DB	481 TTTTGGGGGCCAAGATCAAGTGGGACAGAGACCTGGTGGCAAAATGGGGCCCTTGTGACATC	540
QY	541 TGTAACAAGTATGAGAGATGCTGTGGACAAACCAAGGACCCCTGAGAGACTTCTC	600
DB	541 TGTAACAAGTATGAGAGATGCTGTGGACAAACCAAGGACCCCTGAGAGACTTCTC	600
QY	601 CGAGAGCGGGCAGAGAAAGATGGGCGAAGTCTCAACCGTATTCATACAGAGACATTC	660
DB	601 CGAGAGCGGGCAGAGAAAGATGGGCGAAGTCTCAACCGTATTCATACAGAGACATTC	660
QY	661 TGGAAAGGGGACACCCCGCATCTGGCCCCGAAATGAAACCTTGAACAAACTCTGGCATTT	720
DB	661 TGGAAAGGGGACACCCCGCATCTGGCCCCGAAATGAAACCTTGAACAAACTCTGGCATTT	720
QY	721 GACTTCAACAAGCTTAACTTCTCTGACGAGCTCAACGAGATTCATCTGAGAGCTATGG	780
DB	721 GACTTCAACAAGCTTAACTTCTCTGACGAGCTCAACGAGATTCATCTGAGAGACTATGG	780
QY	781 AAGGGCCGCTGGCAGGGCAATGACATTGTCTGAAGGTCTGAAGGTTTCAGACTGAGT	840
DB	781 AAGGGCCGCTGGCAGGGCAATGACATTGTCTGAAGGTTCTGAAGGTTTCAGACTGAGT	840
QY	841 ACAAGGAAGACAGAGGACTTCAATGAAGAAGTCTCCCGGCTCAGAGATTTTCTGCAATCA	900
DB	841 ACAAGGAAGACAGAGGACTTCAATGAAGAAGTCTCCCGGCTCAGAGATTTTCTGCAATCA	900
QY	901 AATGTCATCCAGTGTAGTGTGCTGACAGTCTCACCTGCTCTCATCTCATCTCTATC	960
DB	901 AATGTCATCCAGTGTAGTGTGCTGACAGTCTCACCTGCTCTCATCTCATCTCTATC	960
QY	961 ACACATCTGATATCCGATATGATCCCTCTTACATGTACTATCAATGAAGGACCAATTTTCTC	1020


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Db 361 ACCCCCTGCACTCTGGACGCGCATGAGACCGTGATATGTACAGAGCTATTGCG 420
Qy 421 TACAAAGCAGACATCAATGCACTGAATGAACAACGGGAATGTGCCCCCTGCACTATCCCTGT 480
Db 421 TACAAAGCAGACATCAATGCACTGAATGAACAACGGGAATGTGCCCCCTGCACTATCCCTGT 480
Qy 481 TTTTGGGGCCAAAGATCAAGTGGCAGAGGACCTGGTGGCAAAATGGGGCCCTTGTGCAGATC 540
Db 481 TTTTGGGGCCAAAGATCAAGTGGCAGAGGACCTGGTGGCAAAATGGGGCCCTTGTGCAGATC 540
Qy 541 TGTAAACAATATGAGAGATGCTGTGAGCAAAAGCCAAAGGACCCCTGAGAGAGCTTTC 600
Db 541 TGTAAACAATATGAGAGATGCTGTGAGCAAAAGCCAAAGGACCCCTGAGAGAGCTTTC 600
Qy 601 CGAGAGCCGGGCGAGAGAAATGGGCGCAATCTCAACCGTATTCCTACACAGACATTC 660
Db 601 CGAGAGCCGGGCGAGAGAAATGGGCGCAATCTCAACCGTATTCCTACACAGACATTC 660
Qy 661 TGGAAAGGGGACACCCGACTCGGCGCGGAAATGGAACCTGGAACAAACACTTGGCAAT 720
Db 661 TGGAAAGGGGACACCCGACTCGGCGCGGAAATGGAACCTGGAACAAACACTTGGCAAT 720
Qy 721 GACTTCAAAACAGCTTAATCTTCTGAGAGAGCTCAACGAGAAATCACTCTGAGAGCTATG 780
Db 721 GACTTCAAAACAGCTTAATCTTCTGAGAGAGCTCAACGAGAAATCACTCTGAGAGCTATG 780
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Db 781 AAGGCGCCCTGGCAGAGGCAATGACATTTGCTGTAAGTGTCTGAGAGCTTGGAGCTGAGT 840
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Db 841 ACAAGGAAGAGAGGAGCTTCAATGAAGTGTCCCGGCTCAGGATTTCTCGGATCCA 900
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Db 901 AATGTGCTCCAGTGTCTAGTGTGCTGCGAGTCTCCACCTGCTCCTCATCTCTCATC 960
Qy 961 ACACACTGGATGCCGTATGATCCCTCTAACAATGTACTACATGAAGGACCAATTTGCTC 1020
Db 961 ACACACTGGATGCCGTATGATCCCTCTAACAATGTACTACATGAAGGACCAATTTGCTC 1020
Qy 1021 GTGGACCAAGAGCCAGGCTGTGAAGTTTGTGTGACATGGAAGGGGCGCTTCTCTCA 1080
Db 1021 GTGGACCAAGAGCCAGGCTGTGAAGTTTGTGTGACATGGAAGGGGCGCTTCTCTCA 1080
Qy 1081 CACACACTAGAGCCCTCATCCACGACATGCACTCAATAGCCGTAGTGAATGATGAT 1140
Db 1081 CACACACTAGAGCCCTCATCCACGACATGCACTCAATAGCCGTAGTGAATGATGAT 1140
Qy 1141 GAGGACATGACTGCCGGAATTAAGCATGGCTGAATGTCATGTCCTGAT 1200
Db 1141 GAGGACATGACTGCCGGAATTAAGCATGGCTGAATGTCATGTCCTGAT 1200
Qy 1201 GAGGACATGACTGCCGGAATTAAGCATGGCTGAATGTCATGTCCTGAT 1260
Db 1201 GAGGACATGACTGCCGGAATTAAGCATGGCTGAATGTCATGTCCTGAT 1260
Qy 1261 CGCATGTATGCACTGCTGGGTAGCCCCGGAAGCTCTGACAGAAAGCCTTGAACACA 1320
Db 1261 CGCATGTATGCACTGCTGGGTAGCCCCGGAAGCTCTGACAGAAAGCCTTGAACACA 1320
Qy 1321 GAGGACATGACTGCCGGAATTAAGCATGGCTGAATGTCATGTCCTGAT 1380
Db 1321 GAGGACATGACTGCCGGAATTAAGCATGGCTGAATGTCATGTCCTGAT 1380
Qy 1381 CTTGGGCTTACCTCCACAGATATTTCCCTCATGTGTGTAAGTCAATGAGTCTGC 1440
Db 1381 CTTGGGCTTACCTCCACAGATATTTCCCTCATGTGTGTAAGTCAATGAGTCTGC 1440
Qy 1441 ATGAATGAAGACCTGCAAAAGGACCAAAATTTGACATGATGTCCTTATGAGAAG 1500
Db 1441 ATGAATGAAGACCTGCAAAAGGACCAAAATTTGACATGATGTCCTTATGAGAAG 1500

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Db 1438 ATGAATGAAGACCTGCAAAAGGACCAAAATTTGACATGATGTCCTTATGAGAAG 1497
Qy 1501 ATGACAGGCAAGTGAAGTGAAGTCTTGTGCTGAATCCAGAGGTGTCCGGACATAGT 1560
Db 1498 ATGACAGGCAAGTGAAGTGAAGTCTTGTGCTGAATCCAGAGGTGTCCGGACATAGT 1557
Qy 1561 TGGGGGAATGCACTCCCAAGAGAGAGGCTCTGTGTGCTCCCGGCTCCAGTAT 1620
Db 1558 TGGGGGAATGCACTCCCAAGAGAGAGGCTCTGTGTGCTCCCGGCTCCAGTAT 1617
Qy 1621 GGTACTACCCAGCTGGGGTTCATCCCTTCCCATCTTCCATCCTGACGAGAGG 1680
Db 1618 GGTACTACCCAGCTGGGGTTCATCCCTTCCCATCTTCCATCCTGACGAGAGG 1677
Qy 1681 GGGGGGCTCAGAGCTTTGTGCTTGGCCATGTGTGTCTCCCAACATGGAGAGATCAGCC 1740
Db 1678 GGGGGGCTCAGAGCTTTGTGCTTGGCCATGTGTGTCTCCCAACATGGAGAGATCAGCC 1737
Qy 1741 CCGCCTGTCACAATTAAGTTATTATGAATAAAAAAAAAAAAAAAAAAAAAA 1789
Db 1738 CCGCCTGTCACAATTAAGTTATTATGAATAAAAAAAAAAAAAAAAAAAAAA 1786

RESULT 4
ACAS6473
ID ACAS6473 standard; cDNA; 1786 BP.
XX
ACAS6473;
XX
06-JUN-2003 (first entry)
XX
Human signalling pathway polynucleotide probe SEQ ID NO 1071.
XX
Human; probe; ss; array element; Parkinson's disease;
XX
signalling pathway population; cancer; adenocarcinoma; leukemia;
XX
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
Homo sapiens.
XX
US650938-B1.
XX
31-DEC-2002.
XX
30-JAN-1998; 98US-0016434.
XX
30-JAN-1998; 98US-0016434.
XX
(INCY-) INCYTE GENOMICS INC.
XX
Au-Young J, Seilhamer J;
XX
WPI; 2003-352189/33.
XX
Combination of polynucleotide probes, useful as array elements in a
XX
microarray for monitoring the expression of a number of target
XX
polynucleotides -
XX
Claim 1; SEQ ID NO 1071; 65bp; English.
XX
The invention relates to a combination which, comprises a number of
XX
polynucleotide probes comprising a sequence selected from one of the 1490
XX
sequences mentioned in the specification. The combination is useful as an
XX
array element in a microarray for monitoring the expression of a number
XX
of target polynucleotides. The microarray is particularly useful in the
XX
diagnosis and treatment of cancer and immunopathology and neuropathology.
XX
The microarray is useful in diagnostics and treatment regimens, drug
XX
discovery and development, toxicological and carcinogenicity studies,
XX
forensics and pharmacogenomics. The microarray is also useful for
XX
monitoring progression of diseases and for developing sophisticated
XX
profiles for the effects of currently available therapeutic drugs. The
XX
combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX
and genomic fragments and in research and diagnostic applications. The
XX
array can detect changes in expression in a large number of genes coding

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CC for different signaling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukemia
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.

XX
 SQ Sequence 1786 BP; 443 A; 486 C; 479 G; 378 T; 0 other;
 Query Match 99.0%; Score 1771.4; DB 25; Length 1786;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 1 GAATTCATCTCTGCACTCTACCGAGGAGTTCCCGAGAGGATCTCGAGCCCGAGT 60
 DB 1 GAATTCATCTCTGCACTCTACCGAGGAGTTCCCGAGAGGATCTCGAGCCCGAGT 60
 QY 61 CCCGAGGATAAAGCTTGGGGTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 DB 61 CCCGAGGATAAAGCTTGGGGTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 QY 121 TCCCAATCCAGGGGACTCGCGCGCGGACGCTGCTATGACGACATTTTCACTCAGTGC 180
 DB 121 TCCCAATCCAGGGGACTCGCGCGCGGACGCTGCTATGACGACATTTTCACTCAGTGC 180
 QY 181 CGGAGGCAACGAGTCCCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 240
 DB 181 CGGAGGCAACGAGTCCCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 240
 QY 241 CAGGGGACGATCATGGCTTCTCCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 300
 DB 241 CAGGGGACGATCATGGCTTCTCCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 300
 QY 301 GTGGTTGAGATGTTGATCATCGGGGGGACCGGATCAATGTAATGAACCGTGGGGATGAC 360
 DB 301 GTGGTTGAGATGTTGATCATCGGGGGGACCGGATCAATGTAATGAACCGTGGGGATGAC 360
 QY 361 ACCCCCTTGCATCTGGGAGCAGTATCGACACCGTGTATTTGTACAGAACTATTGAG 420
 DB 361 ACCCCCTTGCATCTGGGAGCAGTATCGACACCGTGTATTTGTACAGAACTATTGAG 420
 QY 421 TACAGGCGAGACATCAATGCACTGAGTGAATGAACACGGGAATGTCCTTGTGCTGT 480
 DB 421 TACAGGCGAGACATCAATGCACTGAGTGAATGAACACGGGAATGTCCTTGTGCTGT 480
 QY 481 TTTTGGGCGCAAGATCAAGTGGCAGAGACCTGGTGGCAATGGGGCCCTTGTGAGCATC 540
 DB 481 TTTTGGGCGCAAGATCAAGTGGCAGAGACCTGGTGGCAATGGGGCCCTTGTGAGCATC 540
 QY 541 TGTAAACAGTATGGAGAGATGCTGTGACAAAGCAAGGACCCCTGAGAGAGCTTCTC 600
 DB 541 TGTAAACAGTATGGAGAGATGCTGTGACAAAGCAAGGACCCCTGAGAGAGCTTCTC 600
 QY 601 CGAGAGCGGCGAGAGAGATGGCCAGATCTCAACCGTATTCCATACAAGGACACATTC 660
 DB 601 CGAGAGCGGCGAGAGAGATGGCCAGATCTCAACCGTATTCCATACAAGGACACATTC 660
 QY 661 TGGAGGGGACACCCCGCAGTCCGCGCCGAAATGGAACCTTGAACAACTCTGGCAT 720
 DB 661 TGGAGGGGACACCCCGCAGTCCGCGCCGAAATGGAACCTTGAACAACTCTGGCAT 720
 QY 721 GACTTCAACAGCTTAACCTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
 DB 721 GACTTCAACAGCTTAACCTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
 QY 781 AAGGCCCTCGCAGGGCAATGACATCTCTGTAAGGTGCTGAAGGTTGAGAGCTGGAGT 840
 DB 781 AAGGCCCTCGCAGGGCAATGACATCTCTGTAAGGTGCTGAAGGTTGAGAGCTGGAGT 840
 QY 841 ACAAGGAAGACGAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCCA 900
 DB 841 ACAAGGAAGACGAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCCA 900

DB 841 ACAAGGAAGACGAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCCA 900
 QY 901 AATGTGCTCCAGTGTAGGTGCTGCGAGTCTCCAGTCTCTCATCTCTCTCTCTCTCTCT 960
 DB 901 AATGTGCTCCAGTGTAGGTGCTGCGAGTCTCCAGTCTCTCATCTCTCTCTCTCTCTCT 960
 QY 961 ACACACTGGATGCGGTATGGATCCCTCTACAAATGTACTACATGAAGGACCAATTTCTGC 1020
 DB 961 ACACACTGGATGCGGTATGGATCCCTCTACAAATGTACTACATGAAGGACCAATTTCTGC 1020
 QY 1021 GTGACACAGAGCCAGGCTGTGAAGTTTCTTTGGACATGCGAAGGGGATGCGCTTCTCTA 1080
 DB 1021 GTGACACAGAGCCAGGCTGTGAAGTTTCTTTGGACATGCGAAGGGGATGCGCTTCTCTA 1080
 QY 1081 CACACACTAGAGCCCTCATCCACGACATGCTCAATAGCCGTAGTGTATGATTTGAT 1140
 DB 1081 CACACACTAGAGCCCTCATCCACGACATGCTCAATAGCCGTAGTGTATGATTTGAT 1140
 QY 1141 GAGGACATGACTGCGCCGAAATTAGCATGCTCATGTCAAGTTTCTTTTCCAATGCTCTG 1200
 DB 1141 GAGGACATGACTGCGCCGAAATTAGCATGCTCATGTCAAGTTTCTTTTCCAATGCTCTG 1200
 QY 1201 CGCATGTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 DB 1201 CGCATGTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 QY 1261 AACAGACGCTCAGCAGACATGCTGAGTTTTCAGTGTCTTCTGTTGGAACTGGTGAACGG 1320
 DB 1261 AACAGACGCTCAGCAGACATGCTGAGTTTTCAGTGTCTTCTGTTGGAACTGGTGAACGG 1320
 QY 1321 GAGGTACCTTTGCTGACCTCTCCAATATGAGATTTGGAATGAAGGTGGCATTTGGAAGGC 1380
 DB 1321 GAGGTACCTTTGCTGACCTCTCCAATATGAGATTTGGAATGAAGGTGGCATTTGGAAGGC 1380
 QY 1381 CTTGGGCTACCATCCACAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
 DB 1381 CTTGG---TACCATCCACAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1437
 QY 1441 ATGAATGAGAGCCCTGCAAGCGACCCCAATTTGACATGATTTGCTCTATCTTTGAGAAG 1500
 DB 1438 ATGAATGAGAGCCCTGCAAGCGACCCCAATTTGACATGATTTGCTCTATCTTTGAGAAG 1497
 QY 1501 ATGAGGACAAATAGGACTGGAAGGCTCTTCCCTGAACTCCAGAGGTGTCGGGACATGGT 1560
 DB 1498 ATGAGGACAAATAGGACTGGAAGGCTCTTCCCTGAACTCCAGAGGTGTCGGGACATGGT 1557
 QY 1561 TGGGGGAATGCACTTCCCAAGCAGAGGCTCTGTTGCTCTCCCGCTTCCAGTCAAT 1620
 DB 1558 TGGGGGAATGCACTTCCCAAGCAGAGGCTCTGTTGCTCTCCCGCTTCCAGTCAAT 1617
 QY 1621 GGTACTACCCAGGCTGGGGTCCATCCCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCC 1680
 DB 1618 GGTACTACCCAGGCTGGGGTCCATCCCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCC 1677
 QY 1681 GGCGGCTCAGAGCTTTGTCTCTCTGCACTGTCCTCCCAATGTTGCTCCCAATGAGGATCAGCC 1740
 DB 1678 GGCGGCTCAGAGCTTTGTCTCTCTGCACTGTTGCTCCCAATGTTGCTTCCCAATGAGGATCAGCC 1737
 QY 1741 CCGCTGTCACAATAAAGTTTATTATGAAAAAATAAATAAATAAATAAATAAATAAATAA 1789
 DB 1738 CCGCTGTCACAATAAAGTTTATTATGAAAAAATAAATAAATAAATAAATAAATAAATAA 1786

RESULT 5

AAZ33623

ID AAZ33623 standard; cDNA; 1780 BP.

XX

AC AAZ33623;

XX

DT 08-DEC-1999 (first entry)

XX

DE Human breast tumour-associated EST 13.

XX

KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
 KW treatment; tumour; cytostatic; medicament; ss.
 OS Homo sapiens.
 EN DE19813839-A1.
 XX
 XX 23-SEP-1999.
 PD
 XX 20-MAR-1998; 98DE-1013839.
 PE
 XX 20-MAR-1998; 98DE-1013839.
 PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA
 XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 PI WPI; 1999-528981/45.
 DR
 XX Human nucleic acid sequences and protein products from tumor breast
 PT tissue, useful for breast cancer therapy -
 XX
 PS Claim 3; 94; 188pp; German.
 CC This invention describes novel human nucleic acid sequences from tumor
 CC breast tissue which have cytostatic activity. The nucleic acid sequences
 CC can be used to produce and isolate full-length gene sequences. They can
 CC be used to express proteins, which can be used as tools to find an
 CC actively against breast cancer. The sequences can be used in sense or
 CC antisense form. They are especially useful for medicaments for gene
 CC therapy to treat breast cancer. AA23611-248617 represents expressed
 CC sequence tags described in the method of the invention.
 XX
 SQ Sequence 1780 BP; 427 A; 489 C; 492 G; 372 T; 0 other;

Query Match 94.7%; Score 1693.4; DB 20; Length 1780;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 1745; Conservative 0; Mismatches 11; Indels 5; Gaps 4;

QY 24 ACGGAGATTCCCGGAGAGATCTCGACGCCGAGTCCCGAGATTAAGCTTGGGCTTC 83
 DB 14 ACGGATGTTCCCGGAGAGATCTCGACGCCGAGTCCCGAGATTAAGCTTGGGCTTC 73
 QY 84 ATCCCTCTTCCCTGGATCAC-TCCACAGTCTCAGGCTTCCCATTCAGGGGACCTCGGC 142
 DB 74 ATCCCTCTTCCCTGGAGCCGAGTCCCGTCTCAGGCTTCCCATTCAGGGGACCTCGGC 133
 QY 143 GCCGGAGCGTCTATGAGCAGCATTTTCACTCAGTCCGGAGGAGGAGGAGGAGTCCGC 202
 DB 134 GCCGGAGCGTCTATGAGCAGCATTTTCACTCAGTCCGGAGGAGGAGGAGGAGGAGTCCGC 193
 QY 203 TTCCGCTGTGCTGAGCAACACGAGAGAGAGCTTCAACCGAGGGGAGCGATCGCTTCT 262
 DB 194 TTCCGCTGTGCTGAGCAACACGAGAGAGAGCTTCAACCGAGGGGAGCGATCGCTTCT 253
 QY 263 CCCCCCTTGCATCTGGGCTTCCGAGAGGCGGCTTCTGCTGTGAGATGTTGATCATGC 322
 DB 264 CCCCCCTTGCATCTGGGCTTCCGAGAGGCGGCTTCTGCTGTGAGATGTTGATCATGC 313
 QY 323 GGGGGGACGAGTCAATGTAATGAACCGTGGGAGTGAACACCCCTGATCTGGAGGCA 382
 DB 314 GGGGGGACGAGTCAATGTAATGAACCGTGGGAGTGAACACCCCTGATCTGGAGGCA 373
 QY 383 GTCATGACACCGGTATATTGTACAGAGCTATTGCAAGTCAAGGAGGAGCATCAATGCG 442
 DB 374 GTCATGACACCGGTATATTGTACAGAGCTATTGCAAGTCAAGGAGGAGCATCAATGCG 433
 QY 443 TGAATGAACACGGGATGTCCTTGCATATAGCCTTTTGGGGCCCAAGTCAAGTGG 502
 DB 434 TGAATGAACACGGGATGTCCTTGCATATAGCCTTTTGGGGCCCAAGTCAAGTGG 493
 QY 503 CAGAGGACCTGTGCAATGGGCGCTTGTGAGCATCTGTAACAAGTATGAGAGATGC 562
 DB

DB 494 CAGAGGACCTGTGCAAAATGGGCGCTTGTACGATCTGTAACAAGTATGAGAGATGC 553
 QY 563 CTGTGACAAAGCCAGGACCCCTGAGAGAGCTTCTCCGAGAGCGGCGAGAGATGG 622
 DB 554 CTGTGACAAAGCCAGGACCCCTGAGAGAGCTTCTCCGAGAGCGGCGAGAGATGG 613
 QY 623 GCCAGATCTCAACCGTATTTCCATCAAGAGACATTTCTGAAAGGGAGCCACCCGACTC 682
 DB 614 GCCAGATCTCAACCGTATTTCCATCAAGAGACATTTCTGAAAGGGAGCCACCCGACTC 673
 QY 683 GGGCCGAAATGAACCTGAAACAAACCTCTGGCATGACTTCAAAACGTTAATCTTC 742
 DB 674 GGGCCGAAATGAACCTGAAACAAACCTCTGGCATGACTTCAAAACGTTAATCTTC 733
 QY 743 TGACGAACCTCAAGAGATCACTGTGAGAGCTATGAGAGGCGCTGGCAGGCAATG 802
 DB 734 TGACGAACCTCAAGAGATCACTGTGAGAGCTATGAGAGGCGCTGGCAGGCAATG 793
 QY 803 ACATTGTGTGAAGGTGCTGAAGGTTTCGAGACTGAGATCAAGAGAGCAGAGGACTTCA 862
 DB 794 ACATTGTGTGAAGGTGCTGAAGGTTTCGAGACTGAGATCAAGAGAGCAGAGGACTTCA 853
 QY 863 ATGAAGAGTGTCCCGGCTCAGAGATTTTCTGCAATCCAAATGTCTCCGATGTAAGTG 922
 DB 854 ATGAAGAGTGTCCCGGCTCAGAGATTTTCTGCAATCCAAATGTCTCCGATGTAAGTG 913
 QY 923 CCTGCAGTCTCCACTGCTCTCTATCTACTCTATACACATGAGTCCGATAGAT 982
 DB 914 CCTGCAGTCTCCACTGCTCTCTATCTACTCTATACACATGAGTCCGATAGAT 973
 QY 983 CCTGTACAGTATACATGATGAGAGGACCAATTTCTGCTGAGCAGGAGCCAGGCTGTA 1042
 DB 974 CCTGTACAGTATACATGATGAGAGGACCAATTTCTGCTGAGCAGGAGCCAGGCTGTA 1033
 QY 1043 AGTTGCTTTGACATGCGAAGGGGATGCGCTTCTTAACAACACTAAGCCCTCATTC 1102
 DB 1034 AGTTGCTTTGACATGCGAAGGGGATGCGCGCTTCTTAACAACACTAAGCCCTCATTC 1093
 QY 1103 CACGACATGCACTCAATAGCCGTAGTATGATGATGAGAGACATGATCGCGCAATTA 1162
 DB 1094 CACGACATGCACTCAATAGCCGTAGTATGATGATGAGAGACATGATCGCGCAATTA 1153
 QY 1163 GCATGCTGATGTCAGTCTTCTTCCATGTCCTGATGCAATGATGATGATGATGATGAT 1222
 DB 1154 GCATGCTGATGTCAGTCTTCTTCCATGTCCTGATGCAATGATGATGATGATGATGAT 1213
 QY 1223 TAGCCCGGAAAGCTTGTGAGAAAGAGCTGAAAGACAAACAGAGCTTACGAGCATGT 1282
 DB 1214 TAGCCCGGAAAGCTTGTGAGAAAGAGCTTGTGAGAAAGAGCTTACGAGCATGT 1273
 QY 1283 GAGGTTTTCAGTGTCTTGTGGAACCTGATGACAGGAGGATACCTTTTGTGACTTCT 1342
 DB 1274 GAGGTTTTCAGTGTCTTGTGGAACCTGATGACAGGAGGATACCTTTTGTGACTTCT 1333
 QY 1343 CCAATATGAGATGGAATGGAAGGATGGAAGGCTTCCGCTTCAATCCACAG 1402
 DB 1334 CCAATATGAGATGGAATGGAAGGATGGAAGGCTTCCGCTTCAATCCACAG 1392
 QY 1403 GTATTTCCCTCATGTGTGAAGCTCATGAAGATCTGATGAATGAAGACCTTGAAGC 1462
 DB 1393 GTATTTCCCTCATGTGTGAAGCTCATGAAGATCTGATGAATGAAGACCTTGAAGC 1452
 QY 1463 GACCCAAATTTGACATGATTTGTCTTATCTTGAAGATGAGAGCAAGTATGACTGCA 1522
 DB 1453 GACCCAAATTTGACATGATTTGTCTTATCTTGAAGATGAGAGCAAGTATGACTGCA 1512
 QY 1523 AGGTCCTTGCCTGAACCTCAAGGATGAGGAGCATGATGAGGAGGAGCACTCCCAA 1582
 DB 1513 AGGTCCTTGCCTGAACCTCAAGGATGAGGAGCATGATGAGGAGGAGCACTCCCAA 1572
 QY 1583 GCAGAGGCTCTGTGTTGCTTCCCGGCTCAGTCAATGATCAATCCAGGC -TGGGAT 1641
 DB 1573 GCAGAGGCTCTGTGTTGCTTCCCGGCTCAGTCAATGATCAATCCAGGCATGGGAT 1632

|||||CTACATGAGGCACCAATTCGTTGTGACAGAGCCAAGCTGTAAAGTTTTCCTTGGAC 900
QY 1057 ATGGCAAGGGCATGGCTTCCTACACACACTAGAGCCCTCATCCACGACATGCACTC 1116
Db 901 ATGGCAAGAGCGCTGCTTTCTACACACACTAGAGCCCTCATACCTCGACATGCACTA 960
QY 1117 AATAGCCGTAGTGAATGATGATGAGGACATGATGCGCCCAATTTAGCATGGCTGATGTC 1176
Db 961 AATAGCCGTAGTGAATGATGATGAGGACATGATGCGCCCAATTTAGCATGGCTGATGTC 1020
QY 1177 AAGTTCTCTTCCCAATGCTCGCATGATGACCTGCTGGGTAGCCCCCAAGCT 1236
Db 1021 AAGTTCTCTTCCAGTGCAGAGGCGCATGATGACCTGCTGGGTAGCCCCCAAGCC 1080
QY 1237 CTGCAGAGAAGCCTGAAGACACAAACAGACGCTCAGACAGATGTGGAGTTTTCAGTG 1296
Db 1081 CTGCAGAGAAGCCTGAAGACACTAACAGAGCCTCAGACAGATGTGGAGCTTTGCAATG 1140
QY 1297 CTTCTGTGGGAAGCTGACACAGGAGGTACCTTTGCTGACCTCTCCAATATGAGATT 1356
Db 1141 CTTCTGTGGGAAGCTGACACAGGAGGTACCTTTGCTGACCTCTCTTAATATGAGATT 1200
QY 1357 GGAATGAAGGTGGCAATTCGAAGGCTTCGGCTACCATCCACAGGTATTTCCCTCAT 1416
Db 1201 GGAATGAAGGTGGCAATTCGAAGGCTTCGGCTACCATCCACAGGTATTTCCCTCAT 1260
QY 1417 GTGTGTAAGCTATGAAGATCTGCATGAATGAAGACCTCGCAAGCGACCCAAATTTGAC 1476
Db 1261 GTGTGTAAGCTATGAAGATTTGTATGAATGAAGATCTCGCAAGCGATCCAAGTTTGC 1320
QY 1477 ATGATTGTGCTATCTTGAAGATGAGAGATGAGAGCAAGTAG 1515
Db 1321 ATGATTGTGCTATCTTGAAGATGAGAGCAAGTAG 1359

RESULT 8

ABL16569
ID ABL16569 standard; DNA; 1820 BP.
XX
AC ABL16569;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1180.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 1180; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent

capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins
(ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1820 BP; 477 A; 417 C; 479 G; 447 T; 0 other;

Query Match 26.1%; Score 466.8; DB 23; Length 1820;
Best Local Similarity 60.2%; Pred. No. 9.3e-121;
Matches 812; Conservative 0; Mismatches 527; Indels 9; Gaps 2;

QY 157 ATGACGACATTTTCACTCAGTGCAGGAGGCAACGAGTCGCGTTCGCTGTGGCTG 216
Db 171 ATGAGGACATATCCACTGTGCGCGAGGCAACTCGATTCAAGTCGCGCTCTGGTTG 230
QY 217 GACAAACGGAGAACGACCTCAACAGGGGACGATCATGGCTTCTCCCTTTGGACTGG 276
Db 231 GATGAAACGGAGACGACACAATTTGGGAGACCACTGGCTTCAGCCCTTGCATTGG 290
QY 277 GCCTGCCGAGAGGCGCTCTGCTGTGTGAGATGTTGATCATGCGGGGGACGATC 336
Db 291 GTGCTAAAGAGGCGCACGCCAAGCTTGTGAGACTCTGTTGACGCGGTTCCGGTGTG 350
QY 337 AATGTAATGAACCGTGGGGATGACACCCCTGCTGCGAGCGAGTCATGAGACACCGT 396
Db 351 AACGCCACCAATATGGGCGACGACATCCCACTCCATTAGCGGAGCTCATGCGCACCGC 410
QY 397 GATATTGTACAGAAGCTATTGCAGTACAGGCGACATCAATGACAGTGAATGAACCGGG 456
Db 411 GACGTGTCTCAGATGTTGATAAAAGAGCGAGCGATGTGAATGCGGTAAACGAGCATGGA 470
QY 457 AATGTGCCCCCTGCACATATGCTGCTTTTGGGGCCCAAGATCAAGTGGCAGAGGACCTGGTG 516
Db 471 AACACCCCTTGCACATAGCCTGTTTTTGGGGCTATGACATGATCTGCGAGGATCTGCTT 530
QY 517 GCAAATGGGGCCCTTGTGACATCTGTAAACAGATGTGAGAGATGCTCTGTGGACAAAGCC 576
Db 531 AATGGGAGGCCAGGTGGGAATCGCAAAACAGGACGGGCACACACCTCTTTGAAAAGGCC 590
QY 577 AAGGACCCCTGAGAGAGCTTCTCGAGAGCGGCGAGAGAGATGGGCCAAGATCTCAAC 636
Db 591 AAACCCAGTCTGGCCAAAGAGGCTTCAGGATCTTGTAGAAAAGAGCGGAGAGGTTAAG 650
QY 637 CGTATTCCATACAAGGACACATCTTGAAGGGGACCCCGCCTCGGCCCCGAAATGGA 696
Db 651 GTTATCAGCTTCAAGGAACAAGCTGGCAGGGATTTGAAG---ACAGATCCCGGATGCT 707
QY 697 ACCCTGAACAAACACTCTGGCAATTGACTTCAACAGCTTAACTTCTTGACGAAGCTCAAC 756
Db 708 ACTTTGTCCTTCAAGGGAATCAGTATGGAGACCTTAGACCTGCATACCAAGCTGTCG 767
QY 757 GAGAACTACTCTGAGAGCTATGGAAGGCGCTGGCAGGGCAATGACATTTGCTGTGAAG 816
Db 768 GTGACGCGCATCAGGAGAACTTGGCGCGGACGCTGGCAAAAAGACGATGTGTAGCTAAG 827
QY 817 GTGCTGAAGGTTTCGAGACTGGAGTACAAGGAGAGCAGGAGCTTCAATGAAGAGTGTCCC 876
Db 828 ATCTGGCCGTGCTCAGTGCAGCTCGTATATCGCGAGATTTTAAACGAGAGTTTCCC 887
QY 877 CGGCTCAGGATTTTCTCGCATCCAAATGTGCTCCAGTGTAGTGGCTGCGAGCTCTCA 936
Db 888 AAGCTTCGACATCTTTTCGACCCCTAAACATTTTGGCTATTATTGGAGCATGCAATTCGCA 947
QY 937 CTTGCTCTCATCTACTCTCATCACACATGGAATGCGGTATGGATCCCTTACATGTA 996
Db 948 CCCAATCTGGTGACAATT-----AGTCAGTTTATGCCACCGTTCTTCGCTGTGTTAGCCTG 1001


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Oy 997 CTACATGAAGCGCAATTTCTGCTGAGCCAGCCAGCGCTGTGAAGTTTCTTTGGAC 1056
    |||||
Db 1002 CTGCATGAGCACTGGCGCTCTGCTGAGACACACGCGCGGTAAAGCTTTCCTTGAT 1061
Oy 1057 ATGGCAAGGGGCGTGGCTTCTTACACACACTAGAGCCCTTCATCCAGCATGCATC 1116
    |||||
Db 1062 GTTGGAGAGGAATGGCTTCTTCTGCACTGCGAGCGCATTAATTCACATATACCTG 1121
Oy 1117 AATAGCCGTAGTGTATGATATGAGACATGACTGCCGAATTAAGCATGGCTATGTC 1176
    |||||
Db 1122 AACAGTCATCAAGTATGATGACATGATCTGAAGCGCGAATCAACATGGCGCATGTC 1181
Oy 1177 AAGTCTCTTTCCATGTCCTGTGTCATGATGACCTGCTGGGTAGCCCGCAAGCT 1236
    |||||
Db 1182 AATTTCTTTTCCAGAGAGAGAGGAGCATCTTCAACCGGCTTGATGTCGCGAACA 1241
Oy 1237 CTGCAAGAAAGCCCTGAAGACACAAACAGCCCTCAGACAGATGTGAGTTTTCAGTG 1296
    |||||
Db 1242 TTGCAGCCGACAGCGCGATGAAACCTGGAGCGCTGTGACATGTGGAGCTTTGCTATT 1301
Oy 1297 CTCTGTGGGAAGTGTGACACAGGAGTAACTTCTGACCTCTCCATATGAGAT 1356
    |||||
Db 1302 CTTATTTGGAGCTGACTTAACGCGCAGTAACTTCTGCGAGTGTGCGCCATGAGATGC 1361
Oy 1357 GGAATGAAGGTGCGATGGAAGCGCTGCGCTACCATCCACAGATATTTCCCTCAT 1416
    |||||
Db 1362 GGCATGAATAATTCGCTGGAGAGTCTGCGGTCACAGATTTCCGCGAGCATGACGAC 1421
Oy 1417 GTGTGATGCTCATGAAGATCTGATGATGAAGACCCCTGAAGCCCAATTTGAC 1476
    |||||
Db 1422 ATGGCAAGAGTATTTCAATCTGATGATGAAGAGATCCCGGAGAGCGCAAGTTGAC 1481
Oy 1477 ATGATTTGCTCTATCTTGTGAGAAATGC 1504
    |||||
Db 1482 ATGTGTGTTCCCATTTCTGGAGAGATGC 1509
    |||||

```

RESULT 9

AAH09626/c

AAH09626 standard; cDNA; 567 BP.

AAH09626;

26-JUN-2001 (first entry)

Human cDNA clone (3'-primer) SEQ ID NO:6461.

Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens.

EP1074617-A2.

07-FEB-2001.

28-JUL-2000; 2000BP-0116126.

29-JUL-1999; 99JP-0248036.

27-AUG-1999; 99JP-0300253.

11-JAN-2000; 2000JP-0118776.

02-MAY-2000; 2000JP-0183767.

09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -
 XX
 SS Claim 3; SEQ ID 6461; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification, where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH0166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB32446 to
 CC AAB35893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

Sequence 567 BP; 127 A; 141 C; 152 G; 140 T; 7 other;

Query Match 25.2%; Score 451.2; DB 22; Length 567;

Best Local Similarity 92.7%; Pred. No. 1,3e-116; Indels 6; Gaps 5;

Matches 524; Conservative 0; Mismatches 35; Indels 6; Gaps 5;

```

Oy 1207 TATGACCTGCTGCTGAGCCCGAGCCCTGCAAGAAAGCTGAAGACACAAACAGA 1266
    |||||
Db 563 TAAAGANCTGCTGAGGAGCCCGCNAAG-TTGGCCAAAAGCTTAANAACCAACAAAG 505
Oy 1267 CGCTGACAGACATGTGAGTTTTCAGTCTTCTGTGGGAACCTGTACACGGAGGTA 1326
    |||||
Db 504 GTTCAAGNAGACATGTGAAAGTTTTCAMNGCTTCTGTGAAATTTGT-ACAGGAAAGTA 446
Oy 1327 CCTTTGCTGACCTC-TCCAAATATGAGATGGAATGAAGGTGCGATGGAAGCGCTTCG 1385
    |||||
Db 445 CCTTTGCTGACCTTTCCAATATGAGATGGAATGAAGGTGCGATGGAAGCGCTTCG 386
Oy 1386 GCTTACCATCCACAGGATTTTCCCTCATGTGTGAAGCTCATGAAGATCTGCATGA 1445
    |||||
Db 385 GCTTACCATCCACAGGATTTTCCCTCATGTGTGAAGCTCATGAAGATCTGCATGA 326
Oy 1446 TGAAGACCTCTGAAGACCAACCAATTTGACATGATTTGTGCTTATCTTGAGAAATGCA 1505
    |||||
Db 325 TGAAGACCTCTGAAGACCAACCAATTTGACATGATTTGTGCTTATCTTGAGAAATGCA 266
Oy 1506 GGACAAGTAGAGCTGGAAGGTCTTGGCTGGAAGCTCAAGAGGTGCGGACATGTTGGGG 1565
    |||||
Db 265 GGACAAGTAGAGCTGGAAGGTCTTGGCTGGAAGCTCAAGAGGTGCGGACATGTTGGGG 206
Oy 1566 GAATGACCTCTCCCAAGACAGAGCTGTGTTGCTTCCCGGCTCCAGTCATGTATC 1625
    |||||
Db 205 GAATGACCTCTCCCAAGACAGAGCTGTGTTGCTTCCCGGCTCCAGTCATGTATC 146
Oy 1626 TACCCAGGC-TGGGGTCCATCTCTTCCCATCTCTTACCATCTGTG--CGCAAGAGGG 1682
    |||||
Db 145 TACCCAGGCATGTGGGTCCATCTCTTCCCATCTCTTACCATCTGTG--CGCAAGAGGG 86
Oy 1683 CGGGCTGAGAGTTTGTCACTTGCACATGATGTTCTCCCAATGAGGAGGATGAGCC 1742
    |||||
Db 85 CGGGCTGAGAGTTTGTCACTTGCACATGATGTTCTCCCAATGAGGAGGATGAGCC 26
Oy 1743 GCGTGTCAATTAAGTTTATATG 1767
    |||||
Db 25 GCGTGTCAATTAAGTTTATATG 1
    |||||

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RESULT 10
AAA78148/c
ID AAA78148 standard; cDNA; 330 BP.
XX
AC AAA78148;
XX
DT 14-NOV-2000 (first entry)
XX
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:435.
XX
KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
XX immunotherapy; diagnosis; progression; ss.
XX
OS Homo sapiens.
XX
PN WO200037643-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US30909.
XX
PR 23-DEC-1998; 98US-0221298.
XX
PR 02-JUL-1999; 99US-0347496.
XX
PR 22-SEP-1999; 99US-0401064.
XX
PR 19-NOV-1999; 99US-0444242.
XX
PR 02-DEC-1999; 99US-0454150.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yuqiu J;
XX
DR WPI; 2000-442671/38.
XX
XX New colon tumor polypeptides used to inhibit the development of cancer,
XX especially colon cancer, and for diagnosing and monitoring the
XX progression of the cancer -
XX
PS Claim 1; Page 216; 229pp; English.
XX
XX Sequences AAA7722-A78199 represent 478 cDNAs encoding proteins or
XX portions of proteins which are associated with human colon tumours.
XX The invention also specifically discloses 8 human colon tumour proteins
XX (A8B1197-B11904). The nucleic acids, the polypeptides they encode, and
XX such polypeptides may be used in vaccines that target tumour cells,
XX especially colon tumour cells, thereby inhibiting the development of
XX cancer. T-cells specific for the polypeptide expressed by the APC are
XX used to remove tumour cells from biological samples, especially blood or
XX fractions thereof. The sample or the isolated T-cells specific for the
XX polypeptide can then be used to inhibit cancer development. CD4+ and/or
XX CD8+ T-cells from a patient may be incubated with a polypeptide or
XX nucleic acid of the invention, or an APC expressing such a polypeptide,
XX to cause the proliferation of specific T-cells. The T-cells can be
XX cloned and then administered back to the patient to inhibit cancer
XX development. Nucleic acids encoding the polypeptides and antibodies
XX against the polypeptides may be used to determine the expression level
XX of a tumour protein of the invention, and therefore to determine whether
XX cancer cells are present. Such diagnostic methods may also be used to
XX monitor the progression of a cancer by repeating the processes at time
XX intervals, and comparing the current result to previous results. The
XX present sequence represents a cDNA encoding a human colon tumour
XX polypeptide.
XX
SQ Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;
XX
XX Query Match 18.4%; Score 328.4; DB 21; Length 330;
XX Best Local Similarity 99.7%; Pred No. 3.9e-82;
XX Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 996 ACTACATGAGGCACCAATTTGCTGTCGACGAGCCAGCTGTGAAGTTTGGCTTTGGA 1055
|||||
```


PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 1177; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72022).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4354 BP; 1223 A; 902 C; 945 G; 1284 T; 0 other;

Query Match 17.0%; Score 305; DB 23; Length 4354;
Best Local Similarity 56.8%; Pred. No. 5.4e-75;
Matches 642; Conservative 0; Mismatches 430; Indels 59; Gaps 2;

QY 430 GACATCAATGAGTGAATGAACACGGGAATGTGCCCTGCACTATGCTGTTTGGGGC 489
DB 1916 GATGTGAATGCGGTNAACAGCATGGAAACACCCCTGCACTACGCTGTTTGGGGC 1975

QY 490 CAAGATCAAGTGGCAGAGGACCTGGTGGCAAATGGGGCCCTTGTGAGCATCTGTAACAAG 549
DB 1976 TATGACATGATCTGGGAGGATCTGCTTAATGCGGGAGCCAGGTGGGAATCGCAACAAG 2035

QY 550 TATGAGAGATGCTGTGGCAAAAGCCCAAGGACCCCTGAGAGAGCTTCTCGAGAGCGG 609
DB 2036 GACGGGCACACACCTCTTTGAAAGGCCAAACCCAGTCTGGCCAAAGAGGCTTCAGGATCTT 2095

QY 610 GCAGAGAAGATGGGCGCAGAACTCTAACCGTATTCCATACAAGGACACATTTCTGGAAGGG 669
DB 2096 GTAGAAAAGAGCGGCAGAGAGGTTAAGGTTATCAGCTTCAAGGAACAAGCTGGCAGGGA 2155

QY 670 ACCACCCGCACTCGGCCCGGAAATGGAAACCTCTGGAACAAACACTCTGGCAATTGACTTCAA 729
DB 2156 TTGA---AGACGAGATCCCGGATGCTACTTTGTCCCGTTTCAAGGAATCAGTATGGA 2212

QY 730 CAGCTTAATCTCTGACGAAGTCAACGAGAAATCACTCTGGAGAGCTATGGAAGGCCGCG 789
DB 2213 GACCTAGACCTGCATACCAGCTGTGCGGTGAGCCATCAGGAGAACTTGGCGCGGACGC 2272

QY 790 TGGCAGGGCAATGACATTTGCTGTAAGGTGCTGAAGTTTCGAGACTGGAGTACAGGAAG 849
DB 2273 TGGCAAAAGACGATGTGGTAGCTAAGATCTTGGCCGTGCGTCACTGACCGCTCGTATA 2332

QY 850 AGCAGGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTGCATCCAAATGTGCTC 909
DB 2333 TCGCGAGATTTAAGCAGAGGTTTCCCAAGCTTCGCACTCTTTTCGACCCCTAAACATTTTG 2392

QY 910 CCAAGTGTAGTGTGCTGCGAGTCTCCACCTGCTC----- 943
DB 2393 CCTATTATTGGAGCATGCAATTCGCCACCACTCTGGTGACAATTTAGTCAGGTGCGTTGA 2452

QY 944 -----CTCATCTACTCTCATCACACATGGATGC 973
DB 2453 ATTTAAATACTTCAGAAATGACCGTATAAGGTAACCATCTATTCTTTTAGTTATGC 2512

QY 974 CGTATGGATCCCTCTACAATGTACTACATGAAGCACAATTTCTGTCGTGAGCAGAGCC 1033
DB 2513 CACGTTCTTCTGCTGTTAGCCTGTCATGAGCAACTGGCGTCTGTTGAGCAGCAGCC 2572

QY 1034 AGGCTGTCAAGTTTTCCTTTGGACATGCAAGGGGCATGGCTTCTCTACACACATAGAGC 1093
DB 2573 AGCGGTAAAGCTTTGCTTGGATGTTGCGAGAGAAATGGCTTCTCTGACCTCGTGGAGC 2632

QY 1094 CCCTCATCCCACGACATGCACTCAATAGCCGTAGTAAATGATTGATGAGGACATGACTG 1153
DB 2633 GCATTATTCCAAATATACCTTGAAACAGTCACTACGTCATGATCGACGATGATCTGACGG 2692

QY 1154 CCCGAATTAGCATGGCTGATGTCAGTCTCTTTTCCAAATGTCCTGGTCGCAATGTATGCAC 1213
DB 2693 CGAGAATCAACATGGCGGATGCCAAATCTCTTTCCAAGAGAGGAGCGCATCTATCAAC 2752

QY 1214 CTGCTGGGTAGCCCCCGAAGCTCTGCAGAAGAGCCTGAAGACACAACAACAGCGCTCAG 1273
DB 2753 CGGCTTGGATGTCGCGCGAAACATTTGCAGCGCAAGCAGGCGGATCGAAACTGGAGGCT 2812

QY 1274 CAGACATGTGGAGTTTTCAGTGTCTTCTGTGGAACTGGTGCACACGGGAGGTACCTTTG 1333
DB 2813 GTGACATGTGGAGCTTTGCTATTCTTTTGGGAGCTGACTACGCGGAGGTACCTTCG 2872

QY 1334 CTGACCTCTCAATATGAGAGATGGAATGAAGGTGGCAATGGAAGGCTTCGGCTTACCA 1393
DB 2873 CCGAGTGTGCGCCATGGAGTGGCGCATGAAAATTTGGTTGGAAAGGTCTGGGGTCAAGA 2932

QY 1394 TCCACACAGGTATTTCCCTCATGTCGTAAAGCTCATGAAGATCTGCATGAATGAAGACC 1453
DB 2933 TTCCGCCAGGCACATCGACGCACATGGCCAAAGCTGATTTCAATCTGCATGAACGAGGATC 2992

QY 1454 CTGCAAAAGCGACCCAAATTTGACATGATTTGTCCTATCTCTTGAAGAATGC 1504
DB 2993 CCGGCAAGCGGCCCAAGTTCGACATGTTGGTTCCCATTTCTGGAGAAGATGC 3043

RESULT 14
AAH35546
ID AAH35546 standard; cDNA; 568 BP.
XX
AC AAH35546;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2628.
XX
DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 11; ss.
XX
XX Homo sapiens.
OS
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
DR P-PSDB; AAG76141.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 1; Page 4235-4236; 9803pp; English.

CC AAH32943 to AAH31195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH31196 to AAH37204
 CC and AAG77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 568 BP; 148 A; 136 C; 143 G; 129 T; 12 other;

XX Query Match 13.5%; Score 240.8; DB 22; Length 568;
 XX Best Local Similarity 97.2%; Pred. No. 2.4e-57;
 XX Matches 245; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 451 CACGGGAATGTCCTCCATCATGCTGTTTGGGGCAAGATCAAGTGGCAGAGGC 510
 Db 2 CACGGGAATGTCCTCCATCATGCTGTTTGGGGCAAGATCAAGTGGCAGAGGC 61
 QY 511 CTGGTGGCAATGGGGCCCTTGTGAGCATCTGTAAACAAGTATGAGAGTGGCTGTGAC 570
 Db 62 CTGGTGGCAATGGGGCCCTTGTGAGCATCTGTAAACAAGTATGAGAGTGGCTGTGAC 121
 QY 571 AAAGCCAAAGCACCCTTGAAGAGCTTCTCCAGAGCGGGCAGAGAAGTGGGCCAGAA 630
 Db 122 AAAGCCAAAGCACCCTTGAAGAGCTTCTCCAGAGCGGGCAGAGAAGTGGGCCAGAA 181
 QY 631 CTCACCGTATTCATACAGAGACATTCGGAAGGGGACACCCGCACTGGCCCGCA 690
 Db 182 CTCACCGTATTCATACAGAGACATTCGGAAGGGGACACCCGCACTGGCCCGCT 241
 QY 691 AATGGAACTCTG 702
 Db 242 GAGTCACCACTG 253

RESULT 15
 ABX74732/C
 ID ABX74732 standard; cDNA; 285 BP.

XX ABX74732;

XX 21-MAR-2003 (first entry)

DE Human cDNA sequence #55 differentially expressed in CC-RCC types.

XX Human; microarray; solid surface; immobilised probe; CC-RCC;
 KW differential expression profile; aggressive CC-RCC tumour type;
 KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
 KW gene expression profiling; tumour tissue; gene; ss.

OS Homo sapiens.

PN WO200279411-A2.

PD 10-OCT-2002.

XX 29-MAR-2002; 2002MO-US09576.

XX 29-MAR-2001; 2001US-279411P.
 XX (VAND-) VAN ANDEL INST.

XX Haab B, Rhodes D, Teh BT, Takashi M;

XX WPI; 2003-040679/03.

PT New microarray, comprising a matrix of cDNA probe from a set of probes
 PT immobilised to a solid surface in predetermined order, useful in the
 PT prognosis of patients with clear cell renal carcinoma -
 XX
 PS Claim 1; SEQ ID No 386; 179pp; English.

XX The present invention relates to a microarray comprising a matrix of
 CC at least one cDNA probe from a set of probes immobilised to a solid
 CC surface in a predetermined order, where a row of pixels corresponds
 CC to replicates of one distinct probe from the set. The probes are
 CC complementary to nucleic acid sequences that are expressed
 CC differentially in aggressive as compared to non-aggressive types of
 CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
 CC under high stringency conditions. The microarray is useful for the
 CC prognosis of patients with CC-RCC, wherein aggressive and
 CC non-aggressive CC-RCC tumour types are characterised by differential
 CC expression profiles of genes that hybridise with one or more probes
 CC immobilised on the microarray. The arrays are useful for gene
 CC expression profiling of tumour and normal tissues. The present
 CC sequence represents a human cDNA sequence differentially expressed
 CC in aggressive vs. non-aggressive type CC-RCC phenotypes.

XX Sequence 285 BP; 57 A; 72 C; 86 G; 66 T; 4 other;

XX Query Match 12.8%; Score 228.8; DB 25; Length 285;
 XX Best Local Similarity 97.4%; Pred. No. 4.1e-54;
 XX Matches 263; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 1513 TAGAGCTGGAAGGTCCTTGGCTGAATCCAGAGGTGCGGACATGTTGGGGGAATGC 1571
 Db 270 TAGAGCTGGAAGGTCCTTGGCTGAATCCAGAGGTGCGGACATGTTGGGGGAATGC 211
 QY 1572 ACCTCCCAAGACAGACAGGCTTGGTGGCTCCCGCCCTCCAGTCACTGATACCCC 1631
 Db 210 ACCTCCCAAGACAGACAGGCTTGGTGGCTCCCGCCCTCCAGTCACTGATACCCC 151
 QY 1632 AGCC-TGGGGTCCATCCCTTCCCATCCCTTACCATCTG-GCGCAAGAGGGCGGGCTC 1689
 Db 150 AGCCATGGGGTCCATCCCTTCCCATCCCTTACCATCTG-GCGCAAGAGGGCGGGCTC 91
 QY 1690 AGAGCTTGTCACTTGGCCACATGCTGTCTCCCAATATGGAGGATACAGCCCGCTGTC 1749
 Db 90 AGAGCTTGTCACTTGGCCACATGCTGTCTCCCAATATGGAGGATACAGCCCGCTGTC 31
 QY 1750 ACAATTAAGTTTATTAATAAAAAA 1779
 Db 30 ACAATTAAGTTTATTAATAAAAAA 1

Search completed: September 22, 2003, 17:14:38
 Job time : 374 secs

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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: KIN-2C1P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-955-841-1

Query Match 100.0%; Score 1789; DB 3; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATCTGTCGACTGCTACCAAGGAGTTCCCGGAGAGATCTTCGACGCCGAGT 60
DB 1 GAATTCATCTGTCGACTGCTACCAAGGAGTTCCCGGAGAGATCTTCGACGCCGAGT 60
QY 61 CCCGAGGATTAAGCTTGGGGTTTCATCTCTCCCTGATCACTCACAAGTCTGAGGT 120
DB 61 CCCGAGGATTAAGCTTGGGGTTTCATCTCTCCCTGATCACTCACAAGTCTGAGGT 120
QY 121 TCCCAATTCAGAGGAGCTTGCGGCGCCGGAGCGTGTCTATGAGACGACATTTTCACTAGTGC 180
DB 121 TCCCAATTCAGAGGAGCTTGCGGCGCCGGAGCGTGTCTATGAGACGACATTTTCACTAGTGC 180
QY 181 CGGAGGCGCAACGCACTGCGCCCTTGGCTGTGTGACACACGAGAGAACCACTCTCAAC 240
DB 181 CGGAGGCGCAACGCACTGCGCCCTTGGCTGTGTGACACACGAGAGAACCACTCTCAAC 240
QY 241 CAGGGGAGCATGATGAGCTTCTCCCTTGCACCTGGGAGCTGCGAGAGGGCGCTCTGCT 300
DB 241 CAGGGGAGCATGATGAGCTTCTCCCTTGCACCTGGGAGCTGCGAGAGGGCGCTCTGCT 300
QY 301 GTGGTTGAGATGTTGATCATGCGGGGGGCGAGATCAATGTAATGAACCGTGGGATGAC 360
DB 301 GTGGTTGAGATGTTGATCATGCGGGGGGCGAGATCAATGTAATGAACCGTGGGATGAC 360
QY 361 ACCCCCTGCTATCTGCGACGCGCATGAGACCGGTATATTGTACAGAGCTATTGCGAG 420
DB 361 ACCCCCTGCTATCTGCGACGCGCATGAGACCGGTATATTGTACAGAGCTATTGCGAG 420
QY 421 TACAAGGCGAGCATCAATGCAATGCAATGAACGAGGAAATGTCCTTGCATATGCTGT 480
DB 421 TACAAGGCGAGCATCAATGCAATGCAATGAACGAGGAAATGTCCTTGCATATGCTGT 480
QY 481 TTTTGGGGCCAAAGATCAAGTGGCAGAGGACCTGTGGCAAAATGGGGCCCTTGTACAGATC 540
DB 481 TTTTGGGGCCAAAGATCAAGTGGCAGAGGACCTGTGGCAAAATGGGGCCCTTGTACAGATC 540
QY 541 TGTAAACAAGTATGAGAGAGATGCTGTGCAAAAGCCAAAGCCACCTTGAGAGAGCTTCTC 600
DB 541 TGTAAACAAGTATGAGAGAGATGCTGTGCAAAAGCCAAAGCCACCTTGAGAGAGCTTCTC 600
QY 601 CGAGAGCGGGCAGAGAGATGGGCGCAATCTCAACCGTATTCATACAGAGACATTC 660
DB 601 CGAGAGCGGGCAGAGAGATGGGCGCAATCTCAACCGTATTCATACAGAGACATTC 660
QY 661 TGGAGAGGAGCAACCGCACTGGGCGCCGAAATGGAACCTGTAACCAACTCTGGCAAT 720
DB 661 TGGAGAGGAGCAACCGCACTGGGCGCCGAAATGGAACCTGTAACCAACTCTGGCAAT 720

QY 721 GACTTAACAAGCTTAATCTTCTGACGAGCTCAACGAAATCACTCTGAGAGCTATGG 780
DB 721 GACTTAACAAGCTTAATCTTCTGACGAGCTCAACGAAATCACTCTGAGAGCTATGG 780
QY 781 AAGGGCCGCTGGCAGAGGCAATGACATTTGCGTGAAGTGTCTGAAGTTTGGAGCTGAGT 840
DB 781 AAGGGCCGCTGGCAGAGGCAATGACATTTGCGTGAAGTGTCTGAAGTTTGGAGCTGAGT 840
QY 841 ACAAGGAAGAGCAGAGGATCTTCAATGAAGAGTCCCGGGCTCAGAGATTTTCTGGATCCA 900
DB 841 ACAAGGAAGAGCAGAGGATCTTCAATGAAGAGTCCCGGGCTCAGAGATTTTCTGGATCCA 900
QY 901 AATGTCCTCCAGTCTGATGAGTCCCTCTCAATGATGATCAATGAAGGACCAATTTGCTC 960
DB 901 AATGTCCTCCAGTCTGATGAGTCCCTCTCAATGATGATCAATGAAGGACCAATTTGCTC 960
QY 961 ACACATGATGATGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 ACACATGATGATGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GTGACACAGGCGCAGGCTGTGAAGTTTCTTGGACATGCGCAAGGGGCGATGGCTTCTTA 1080
DB 1021 GTGACACAGGCGCAGGCTGTGAAGTTTCTTGGACATGCGCAAGGGGCGATGGCTTCTTA 1080
QY 1081 CACACACTAGAGCCCTCATCCACGACATGACATCAATAGCCGTATGATGATGATGAT 1140
DB 1081 CACACACTAGAGCCCTCATCCACGACATGACATCAATAGCCGTATGATGATGATGATGAT 1140
QY 1141 GAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 GAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 CGCATGTATGACATGCTGCTGGGTAGCCCCCGAAGCTTTCGACAGAGAGCTTGAACACA 1260
DB 1201 CGCATGTATGACATGCTGCTGGGTAGCCCCCGAAGCTTTCGACAGAGAGCTTGAACACA 1260
QY 1261 AACAGAGCTCAGCAGACATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 AACAGAGCTCAGCAGACATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 GAGGTACCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GAGGTACCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 CTTGGGCTTACCATCCACAGATATTTTCCCTCATGTTGTGATGATGATGATGATGAT 1440
DB 1381 CTTGGGCTTACCATCCACAGATATTTTCCCTCATGTTGTGATGATGATGATGATGAT 1440
QY 1441 ATGAATGAAGACCTGCAAGAGGACCAATTTTGAATGATGATGATGATGATGATGATGAT 1500
DB 1441 ATGAATGAAGACCTGCAAGAGGACCAATTTTGAATGATGATGATGATGATGATGATGAT 1500
QY 1501 ATGCAAGCAAGTGAAGCTGGAAGGCTTGTGCTGAATCTCCAGAGGTGTCGGAGATGAT 1560
DB 1501 ATGCAAGCAAGTGAAGCTGGAAGGCTTGTGCTGAATCTCCAGAGGTGTCGGAGATGAT 1560
QY 1561 TGGGGGAATGACCTTCCCAAGAGAGGCTTGTGCTGCTTCCCAAGCTTCCAGATCAT 1620
DB 1561 TGGGGGAATGACCTTCCCAAGAGAGGCTTGTGCTGCTTCCCAAGCTTCCAGATCAT 1620
QY 1621 GGTACTACCCAGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 GGTACTACCCAGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 GCGGGGCTCAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 GCGGGGCTCAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 CCGCTGTGACATTAAGTTTATTAATGAAAAAATGAAAAAATGAAAAAATGAAAAAAT 1789
DB 1741 CCGCTGTGACATTAAGTTTATTAATGAAAAAATGAAAAAATGAAAAAATGAAAAAAT 1789

RESULT 3

RESOUR 3
US-09-390-425-1

US-09-390-423-1
: Sequence 1. Application US/09390425

; Sequence 1, 6338958
; Patent No. 6338958

; FACILE NO. 6338938
: GENERAL INFORMATION:

APPLICANT: Dedhar. Shoukat

APPLICANT: Hannigan, Greg

TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses

; TITLE OF INVENTION: INJECTABLE
; FILE REFERENCE: KIN-2CON

FILE REFERENCE: KIN-ZCON
CURRENT APPLICATION NUMBER: US/09/390.425

CURRENT AFFILIATION NUMBER: 057
CURRENT FILING DATE: 1999-09-03

CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US60/009,074

EARLIER FILING DATE: 1995-12-21

EARLIER FILING DATE: 1999 12 21
: EARLIER APPLICATION NUMBER: US08/752,345

EARLIER FILING DATE: 1996-11-19

EARLIER FILING DATE: 1998
NUMBER OF SEQ ID NOS: 16

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEO for Windows Version 4.0.0; SOFTWARE: L
; SEQ ID NO: 1

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; SEQ ID NO 1
:   LENGTH: 1789

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; LENGTH: 1
; TYPE: DNA

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TYPE: DNA
ORGANISM: H sapiens

ORGANISM: H. sapientiae
FEATURE:

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; FEATURE:
: NAME/KEY: CDS

```

```

; NAME/KEY: CDS
: LOCATION: (157) (1512)

```

LOCATIONS: (1577).
NAME/KEY: Other

```

; NAME/KEY: OULIER
; LOCATION: (0) (0) (0)

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; LOCATION: 115-09-390-425-1

Query Match 100.0%; Score 1789; DB 4; Length 1789;

Best Local Similarity 100.0%; Pred. No. 0;

Base local similarity 100.00; Recd. No.: 0;
Matches 1789; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

1	GAATTCACTGTGCAGTCTTACACACGGAGTTCCTCCGGAGAGAGATCCTGCAGCCCGAGT	60
1	GAATTCACTGTGCAGTCTTACACACGGAGTTCCTCCGGAGAGAGATCCTGCAGCCCGAGT	60
61	CCCGAGATAAAGCTTGGGGTTATCTCTCTTCCCTGGATCACTCCACAGTCCCTCAGGCT	120
61	CCCGAGATAAAGCTTGGGGTTATCTCTCTTCCCTGGATCACTCCACAGTCCCTCAGGCT	120
121	TCCCCAATCAGGGGATCTCGGCGCCGGACGCTGCTATGGACGACATTTTTCACCTCAGTGC	180
121	TCCCCAATCAGGGGATCTCGGCGCCGGACGCTGCTATGGACGACATTTTTCACCTCAGTGC	180
181	CGGAGGGCAACCGAGTGCCTGTCGCTGGCTGGACACCGAGAGACGACTCAAC	240
181	CGGAGGGCAACCGAGTGCCTGTCGCTGGCTGGACACCGAGAGACGACTCAAC	240
241	CAGGGGACGATCATGGCTTCTCCCTCTTGACCTGGGCTGCCAGAGGGCGCTCTGCT	300
241	CAGGGGACGATCATGGCTTCTCCCTCTTGACCTGGGCTGCCAGAGGGCGCTCTGCT	300
301	GTGTTTGAGATGTTGATCATCGCGGGGCGACGGATCAATGPAATGAACCGTGGGGATGAC	360
301	GTGTTTGAGATGTTGATCATCGCGGGGCGACGGATCAATGPAATGAACCGTGGGGATGAC	360
361	ACCCCCCTGCATCTGGCAGCCAGTCACTGGACACCGTGTATTTGTACAGAACTATTGCAG	420
361	ACCCCCCTGCATCTGGCAGCCAGTCACTGGACACCGTGTATTTGTACAGAACTATTGCAG	420
421	TACAAGGCAGACATCAATGCAATGAATGAACACGGGAATGCCCCCTGCACATGACCTGT	480
421	TACAAGGCAGACATCAATGCAATGAATGAACACGGGAATGCCCCCTGCACATGACCTGT	480
481	TTTTTGGGGCCAAAGTCAAGTGGCAGAGGACCTGTGTGGCAAAATGGGGCCCTTGTGACGATC	540
481	TTTTTGGGGCCAAAGTCAAGTGGCAGAGGACCTGTGTGGCAAAATGGGGCCCTTGTGACGATC	540
541	TGTAAACAAGTATCGAGAGATGCCTGTGGACAAACCAAGGCACCCCTGAGAGAGCTTCTC	600
541	TGTAAACAAGTATCGAGAGATGCCTGTGGACAAACCAAGGCACCCCTGAGAGAGCTTCTC	600
601	CGAGAGCGGCAGAGAAAGATGGGGCCAGAACTCTAACCGTATTTCCATACAAGGACACATTC	660

Db 1681 GCGGGCTCAGAGCTTTGTCACTTGCACATGCTGTCTCCCAACATGGAGGATCAGCC 1740
Qy 1741 CCGCTGTCACTATAAGTTTATTTATGAAAAAAAAAAAAAAAAAAAA 1789
Db 1741 CCGCTGTCACTATAAGTTTATTTATGAAAAAAAAAAAAAAAAAAAA 1789

RESULT 4
US-09-566-906-1
Sequence 1, Application US/09566906
Patent No. 6369205
GENERAL INFORMATION:
APPLICANT: Dedhar, Shoukat
APPLICANT: Hannigan, Greg
TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
FILE REFERENCE: KIN-2CON
CURRENT APPLICATION NUMBER: US/09/566,906
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 09/390,425
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US08/752,345
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1789
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157)...(1512)
NAME/KEY: Other
LOCATION: (0)...(0)
US-09-566-906-1

Query Match 100.0%; Score 1789; DB 4; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCATCTGTGCACTGCTACACAGGAGTCCCGGAGAAAGATCTCGACGCCGAGT 60
Db 1 GAATTCATCTGTGCACTGCTACACAGGAGTCCCGGAGAAAGATCTCGACGCCGAGT 60
Qy 61 CCCGAGATTAAGCTTTGGGCTTATCTCTCTCCCTGATCACTCAAGTCTTCAAGCT 120
Db 61 CCCGAGATTAAGCTTTGGGCTTATCTCTCTCCCTGATCACTCAAGTCTTCAAGCT 120
Qy 121 TCCCAATCCAGGGAGCTCGGGCGGGGACGCTGATGAGACATTTTCACTGAGTGC 180
Db 121 TCCCAATCCAGGGAGCTCGGGCGGGGACGCTGATGAGACATTTTCACTGAGTGC 180
Qy 181 CCGGAGGCAACGCAAGTGCCTGCTGCTGCTGCAACACGAGAACGACCTCAAC 240
Db 181 CCGGAGGCAACGCAAGTGCCTGCTGCTGCTGCAACACGAGAACGACCTCAAC 240
Qy 241 CAGGGGAGCATGATGCTTCTCCCTTGCACCTGGGCTCGGAGAGGCGCTCTGCT 300
Db 241 CAGGGGAGCATGATGCTTCTCCCTTGCACCTGGGCTCGGAGAGGCGCTCTGCT 300
Qy 301 GTGGTGAAGATGTTATCATGCGGGGGGACGGATCAATGTAATAACCGTGGGATGAC 360
Db 301 GTGGTGAAGATGTTATCATGCGGGGGGACGGATCAATGTAATAACCGTGGGATGAC 360
Qy 361 ACCCCCTGATCTGGACGCGAGTATGACACCGTGATTTGTAACAGAGCTATTGGAG 420
Db 361 ACCCCCTGATCTGGACGCGAGTATGACACCGTGATTTGTAACAGAGCTATTGGAG 420
Qy 421 TACAAAGCAGACATCAATGCAAGTGAATGAACAGGGAATGTCCTCTGACTATCTGT 480
Db 421 TACAAAGCAGACATCAATGCAAGTGAATGAACAGGGAATGTCCTCTGACTATCTGT 480
Qy 481 TTTTGGGGCAAGATCAAGTGGCAGAGGACCTGTGGCAATGGGGCCCTTTCAGCATC 540
Db 481 TTTTGGGGCAAGATCAAGTGGCAGAGGACCTGTGGCAATGGGGCCCTTTCAGCATC 540

Db 481 TTTTGGGGCAAGATCAAGTGGCAGAGGACCTGTGGCAATGGGGCCCTTTCAGCATC 540
Qy 541 TGTAAAGATATGAGAGATGCTCTGTGACAAAGCCAAAGGACCCCTTGAAGAGTTCTC 600
Db 541 TGTAAAGATATGAGAGATGCTCTGTGACAAAGCCAAAGGACCCCTTGAAGAGTTCTC 600
Qy 601 CGAGCGGGGAGAGATGAGTGGCCAGAACTCAACCGCTATTTCATACAGAGACATTTC 660
Db 601 CGAGCGGGGAGAGATGAGTGGCCAGAACTCAACCGCTATTTCATACAGAGACATTTC 660
Qy 661 TGAAGGGGACACCCGCACTCGGCCCGGAATGGAACCTTGAAACAACTCTGGCAT 720
Db 661 TGAAGGGGACACCCGCACTCGGCCCGGAATGGAACCTTGAAACAACTCTGGCAT 720
Qy 721 GACTTCAACAGCTTAACTTCTCTGCAAGCTCAACGAAATCACTCTGAGAGCTATGG 780
Db 721 GACTTCAACAGCTTAACTTCTCTGCAAGCTCAACGAAATCACTCTGAGAGCTATGG 780
Qy 781 AAGGGCGCTGGCAGGGGCAATGACATTTGTGGAAAGGTGTAAGGTTGAGACTGAGT 840
Db 781 AAGGGCGCTGGCAGGGGCAATGACATTTGTGGAAAGGTGTAAGGTTGAGACTGAGT 840
Qy 841 ACAAGGAAGACAGGAGCTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCA 900
Db 841 ACAAGGAAGACAGGAGCTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCA 900
Qy 901 AATGTGCTCCAGTGTCTGAGTGTGCTGCTGCAAGTCTCACTCTCATCTCACTATC 960
Db 901 AATGTGCTCCAGTGTCTGAGTGTGCTGCTGCAAGTCTCACTCTCATCTCACTATC 960
Qy 961 ACACACTGAGTGGCGTATGATATCCCTCAACATGACTCAATGAAGGACCAATTGCTC 1020
Db 961 ACACACTGAGTGGCGTATGATATCCCTCAACATGACTCAATGAAGGACCAATTGCTC 1020
Qy 1021 GTGACACAGAGCCAGGCTGTGAAGTTTCTTGTGACATGAGGAGGAGCTTCTCTTA 1080
Db 1021 GTGACACAGAGCCAGGCTGTGAAGTTTCTTGTGACATGAGGAGGAGCTTCTCTTA 1080
Qy 1081 CACACACTAGAGCCCTCATCTCCACGACATCACTCAATAGCCGTAATGATGAT 1140
Db 1081 CACACACTAGAGCCCTCATCTCCACGACATCACTCAATAGCCGTAATGATGAT 1140
Qy 1141 GAGGACATGACTGCCGGAATTAAGATGAGTGTGATGATGATGATGATGATGAT 1200
Db 1141 GAGGACATGACTGCCGGAATTAAGATGAGTGTGATGATGATGATGATGATGAT 1200
Qy 1201 CGCATGTATGACCTGCTGGGTAGCCCCGAGGCTTGCAGAGAGCTTGCAGAGAGCT 1260
Db 1201 CGCATGTATGACCTGCTGGGTAGCCCCGAGGCTTGCAGAGAGCTTGCAGAGAGCT 1260
Qy 1261 AACAGACGCTCAGCAGACATGTGAAGTTTGCAGTCTTCTGTGGAACTGGTGAACGG 1320
Db 1261 AACAGACGCTCAGCAGACATGTGAAGTTTGCAGTCTTCTGTGGAACTGGTGAACGG 1320
Qy 1321 GAGGTACCTTTTGTGACCTCTCCAAATGAGATGGAATGAAGAGTGGCAATGGAAGC 1380
Db 1321 GAGGTACCTTTTGTGACCTCTCCAAATGAGATGGAATGAAGAGTGGCAATGGAAGC 1380
Qy 1381 CTTGGGCTTACCATCCACAGTATTTCCCTCATGTGTGTAAAGCTCATGAAGTCTGC 1440
Db 1381 CTTGGGCTTACCATCCACAGTATTTCCCTCATGTGTGTAAAGCTCATGAAGTCTGC 1440
Qy 1441 ATGAATGAAGACCTTGCAAGACGCAAAATTTGACATGATTTGCTTATCTTGAGAG 1500
Db 1441 ATGAATGAAGACCTTGCAAGACGCAAAATTTGACATGATTTGCTTATCTTGAGAG 1500
Qy 1501 ATGCAAGCAAGTGAAGATGGAAGTCTTTCCTGAATCCAGAGGTTCGGGACATGCT 1560
Db 1501 ATGCAAGCAAGTGAAGATGGAAGTCTTTCCTGAATCCAGAGGTTCGGGACATGCT 1560
Qy 1561 TGGGGGAATGCACTCCCAAGCAGAGGCTCTGTGTTGCTCCCGGCTCCAGTAT 1620
Db 1561 TGGGGGAATGCACTCCCAAGCAGAGGCTCTGTGTTGCTCCCGGCTCCAGTAT 1620

QY 1621 GGTACTACCCAGCCTGGGTCATCCCTTCCCATCCCTACCACTGTGCGAAGAGG 1680
DB 1621 GGTACTACCCAGCCTGGGTCATCCCTTCCCATCCCTACCACTGTGCGAAGAGG 1680
QY 1681 GCGGGCTCAGAGCTTTGTCACTTGCCACATGGTGTCTCCCAACATGGGAGGATCAGCC 1740
DB 1681 GCGGGCTCAGAGCTTTGTCACTTGCCACATGGTGTCTCCCAACATGGGAGGATCAGCC 1740
QY 1741 CCGCTGTCAACAATAAGTTTATATGAAAAAATAAAAAAAAAAAAAA 1789
DB 1741 CCGCTGTCAACAATAAGTTTATATGAAAAAATAAAAAAAAAAAAAA 1789

RESULT 5
US-09-428-219-3
; Sequence 3, Application US/09428219
; Patent No. 6177273
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
; FILE REFERENCE: RTS-0101
; CURRENT APPLICATION NUMBER: US/09/428,219
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 1789
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(1515)
US-09-428-219-3

Query Match 99.9%; Score 1787.4; DB 3; Length 1789;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATTCATCTGCTGACTGCTACCGGGAGTTCCCGGAGAGGATCCCTGAGGCCGAGT 60
DB 1 GAAATTCATCTGCTGACTGCTACCGGGAGTTCCCGGAGAGGATCCCTGAGGCCGAGT 60
QY 61 CCCGAGGATAAAGCTTGGGTTTCATCTCCCTGCTGATCACTCCAGATCCTCAGGCT 120
DB 61 CCCGAGGATAAAGCTTGGGTTTCATCTCCCTGCTGATCACTCCAGATCCTCAGGCT 120
QY 121 TCCCAATCCAGGGACTCGGCGCGGAGCGTGCTATGGACGACATTTTCACTCAGTGC 180
DB 121 TCCCAATCCAGGGACTCGGCGCGGAGCGTGCTATGGACGACATTTTCACTCAGTGC 180
QY 181 CCGGAGGGCAACGAGTCGCGTTCGCTTGGCTGGACACACGAGAAACGACCTCAAC 240
DB 181 CCGGAGGGCAACGAGTCGCGTTCGCTTGGCTGGACACACGAGAAACGACCTCAAC 240
QY 241 CAGGGGACGATCATGGCTTCTCCCTTGGCACTGGGCTCGCGAGAGGGCGCTCTGCT 300
DB 241 CAGGGGACGATCATGGCTTCTCCCTTGGCACTGGGCTCGCGAGAGGGCGCTCTGCT 300
QY 301 GTGGTTGAGATGTTGATCATCGGGGGGACGAGTCAATGTAATGAACCGTGGGATGAC 360
DB 301 GTGGTTGAGATGTTGATCATCGGGGGGACGAGTCAATGTAATGAACCGTGGGATGAC 360
QY 361 ACCCCCTGTCATCTGGGAGCCAGTCATGGACACCGTGATATGTACAGAGCTATTGAG 420
DB 361 ACCCCCTGTCATCTGGGAGCCAGTCATGGACACCGTGATATGTACAGAGCTATTGAG 420
QY 421 TACAGGCGACATCAATGCAAGTGAATGAACACGGGAATGTGCCCTGCATCTATCCCTGT 480
DB 421 TACAGGCGACATCAATGCAAGTGAATGAACACGGGAATGTGCCCTGCATCTATCCCTGT 480
QY 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGGACCTTGGTGGCAAAATGGGGCCCTTGTTCAGCATC 540
DB 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGGACCTTGGTGGCAAAATGGGGCCCTTGTTCAGCATC 540

DB 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGGACCTTGGTGGCAAAATGGGGCCCTTGTTCAGCATC 540
QY 541 TGTAAACAGTATGAGAGATGCTTGTGACAAAGCCAAAGCCACCCCTTGAGAGAGCTTCTC 600
DB 541 TGTAAACAGTATGAGAGATGCTTGTGACAAAGCCAAAGCCACCCCTTGAGAGAGCTTCTC 600
QY 601 CGAGAGCGGGCAGAGAGATGGGCGCAGAACTCTCAACCGTATTTCATACAAGGACACATTC 660
DB 601 CGAGAGCGGGCAGAGAGATGGGCGCAGAACTCTCAACCGTATTTCATACAAGGACACATTC 660
QY 661 TGGAGGGGACCCACCCGACCTCGGCCCGAAATGGAACTCTGGAACAACTCTGGCATT 720
DB 661 TGGAGGGGACCCACCCGACCTCGGCCCGAAATGGAACTCTGGAACAACTCTGGCATT 720
QY 721 GACTTCAAAAGCTTAACTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
DB 721 GACTTCAAAAGCTTAACTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
QY 781 AAGGCGCGCTGGCAGGCAATGACATTTCTGTAAGGTGCTGAAGGTTTCGAGACTGAGT 840
DB 781 AAGGCGCGCTGGCAGGCAATGACATTTCTGTAAGGTGCTGAAGGTTTCGAGACTGAGT 840
QY 841 ACAAGGAGAGCAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCA 900
DB 841 ACAAGGAGAGCAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCA 900
QY 901 AATGTCTCCAGTGTAGTGTGCTGACGCTCTCCAGTGTCTCCAGTGTCTCTCTCTCTCATC 960
DB 901 AATGTCTCCAGTGTAGTGTGCTGACGCTCTCCAGTGTCTCCAGTGTCTCTCTCTCTCATC 960
QY 961 ACACACTGGATGCGGTATGGATCCCTCTACAATGACTTACATGAAGGACCAATTTCTGTC 1020
DB 961 ACACACTGGATGCGGTATGGATCCCTCTACAATGACTTACATGAAGGACCAATTTCTGTC 1020
QY 1021 GTGACACGAGCCAGGCTGAAAGTTTCTTTGACATGGCAAGGGGATGGCCTTCTCTA 1080
DB 1021 GTGACACGAGCCAGGCTGAAAGTTTCTTTGACATGGCAAGGGGATGGCCTTCTCTA 1080
QY 1081 CACACACTAGAGCCCTCATCCACGACATGCATCAATAGCCGTAGTGTATGATTTGAT 1140
DB 1081 CACACACTAGAGCCCTCATCCACGACATGCATCAATAGCCGTAGTGTATGATTTGAT 1140
QY 1141 GAGGACATGACTGCGCGAATTAGCATGGCTGATGCTCAAGTTCTCTTTTCCAATGCTCTGGT 1200
DB 1141 GAGGACATGACTGCGCGAATTAGCATGGCTGATGCTCAAGTTCTCTTTTCCAATGCTCTGGT 1200
QY 1201 CGCATGTATGCACTGCTGGTATGCCCCGAACTCTGCAAGAAAGACCTGAAAGACACA 1260
DB 1201 CGCATGTATGCACTGCTGGTATGCCCCGAACTCTGCAAGAAAGACCTGAAAGACACA 1260
QY 1261 AACAGACGCTCAGAGACATGTGGAGTTTTCAGTGTCTTGTGGGAACTGGTGACACGG 1320
DB 1261 AACAGACGCTCAGAGACATGTGGAGTTTTCAGTGTCTTGTGGGAACTGGTGACACGG 1320
QY 1321 GAGGTACCCCTTGTGCTGACCTCTCCAATATGAGATTTGGAATGAAGGTGGCAATTTGGAAGGC 1380
DB 1321 GAGGTACCCCTTGTGCTGACCTCTCCAATATGAGATTTGGAATGAAGGTGGCAATTTGGAAGGC 1380
QY 1381 CTTGGGCTACCATCCCAAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
DB 1381 CTTGGGCTACCATCCCAAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
QY 1441 ATGAATGAAGACCTGCAAGGAGCCCAAAATTTTCAGATGTTGCTTATCTCTTGGAGAG 1500
DB 1441 ATGAATGAAGACCTGCAAGGAGCCCAAAATTTTCAGATGTTGCTTATCTTGGAGAG 1500
QY 1501 ATGAGGACAAAGTAGGACTGGAAGGTCTTCCCTGAACTCCAGAGGTGTCTGGGACATGGT 1560
DB 1501 ATGAGGACAAAGTAGGACTGGAAGGTCTTCCCTGAACTCCAGAGGTGTCTGGGACATGGT 1560
QY 1561 TGGGGGAATGCACTTCCCAAGAGGAGGCTCTGGTGTGCTTCCCGCTTCCAGTCAAT 1620
DB 1561 TGGGGGAATGCACTTCCCAAGAGGAGGCTCTGGTGTGCTTCCCGCTTCCAGTCAAT 1620

QY 1621 GGTAACACCCAGCCGTTGCTCCATCCCTTCCCATCTTACCACTGTGCGAAGAG 1680
 DB 1621 GGTAACACCCAGCCGTTGCTCCATCCCTTCCCATCTTACCACTGTGCGAAGAG 1680
 QY 1681 GCGGAGCTCAGAGCTTTGTCTACTTGCACATGCTGTCTCCCAATGGAAGGATCAGCC 1740
 DB 1681 GCGGAGCTCAGAGCTTTGTCTACTTGCACATGCTGTCTCCCAATGGAAGGATCAGCC 1740
 QY 1741 CCGCTGTCAATAAGTTATTTATGAAAAAAAAAAAAAAAAAAAAA 1789
 DB 1741 CCGCTGTCAATAAGTTATTTATGAAAAAAAAAAAAAAAAAAAAA 1789

RESULT 6
 US-09-016-434-1071
 ; Sequence 1071, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1071:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1786 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: g1146128
 ; US-09-016-434-1071

Query Match 99.0%; Score 1771.4; DB 4; Length 1786;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 GAATTCATGTGCTGCTACACGAGGAGTCCCGGAGAGAGATCCCTGACCGCCGAGT 60
 DB 1 GAATTCATGTGCTGCTACACGAGGAGTCCCGGAGAGAGATCCCTGACCGCCGAGT 60
 QY 61 CCGGAGATTAAGCTTGGGCTTCATCTCTCCCTGTGATCACTCCAGTCTCAGGCT 120
 DB 61 CCGGAGATTAAGCTTGGGCTTCATCTCTCCCTGTGATCACTCCAGTCTCAGGCT 120

QY 121 TCCCAATCCAGGGGACTCGGGCCGAGGACGCTGCTATGAGACATTTTCACTCAGTGC 180
 DB 121 TCCCAATCCAGGGGACTCGGGCCGAGGACGCTGCTATGAGACATTTTCACTCAGTGC 180
 QY 181 CCGGAGGCGCAACGAGTCCGCTTGCCTGTGCTGCAACAACCGAGAGACGACTCAAC 240
 DB 181 CCGGAGGCGCAACGAGTCCGCTTGCCTGTGCTGCAACAACCGAGAGACGACTCAAC 240
 QY 241 CAGGGGAGACGATCATGCTTCTCTCCCTTGTGCACTGGGCTTCCGAGAGGCTCTGCT 300
 DB 241 CAGGGGAGACGATCATGCTTCTCTCCCTTGTGCACTGGGCTTCCGAGAGGCTCTGCT 300
 QY 301 GTGTTGATGATTTATCATGCGGGGGGACGAGATCAATGATATGACCGTGGGATAC 360
 DB 301 GTGTTGATGATTTATCATGCGGGGGGACGAGATCAATGATATGACCGTGGGATAC 360
 QY 361 ACCCCCTGCATCTTGGCAGCAGATGAGACACCTGATATTTGACAGAGCTATTGAG 420
 DB 361 ACCCCCTGCATCTTGGCAGCAGATGAGACACCTGATATTTGACAGAGCTATTGAG 420
 QY 421 TACAAGCAGACATCAATGACGTGAATGAACACGAGAAATGTGCCCTGCATGCTCTGT 480
 DB 421 TACAAGCAGACATCAATGACGTGAATGAACACGAGAAATGTGCCCTGCATGCTCTGT 480
 QY 481 TTTTGGGGCCCAAGATCACTGCGCAGAGACCTGTGTGGAATTTGGGGCCCTGTGAGCATC 540
 DB 481 TTTTGGGGCCCAAGATCACTGCGCAGAGACCTGTGTGGAATTTGGGGCCCTGTGAGCATC 540
 QY 541 TGTAACTAGTATGAGAGATGCTGTGACAAAGCCAGGACACCCCTGAGAGAGCTTCTC 600
 DB 541 TGTAACTAGTATGAGAGATGCTGTGACAAAGCCAGGACACCCCTGAGAGAGCTTCTC 600
 QY 601 CGAGAGCGGGGACAGAGATGGGCCAGATTTCAACCGTATTTCAATACAGAGACATTT 660
 DB 601 CGAGAGCGGGGACAGAGATGGGCCAGATTTCAACCGTATTTCAATACAGAGACATTT 660
 QY 661 TGGAGGGGACCAACCCGACCTCGGCCGGAATGGAACCTGTGAACAAACACTCTGGCAT 720
 DB 661 TGGAGGGGACCAACCCGACCTCGGCCGGAATGGAACCTGTGAACAAACACTCTGGCAT 720
 QY 721 GACTTCAACAGCTTAACTTCTCTGACGAGCTCAACGAGAACTCTGTGAGAGCTATG 780
 DB 721 GACTTCAACAGCTTAACTTCTCTGACGAGCTCAACGAGAACTCTGTGAGAGCTATG 780
 QY 781 AAGGCGCTGCGCAGGAGCAATGACATTTGCTGAAGGTGCTGAAGCTTGAAGCTGAGT 840
 DB 781 AAGGCGCTGCGCAGGAGCAATGACATTTGCTGAAGGTGCTGAAGCTTGAAGCTGAGT 840
 QY 841 ACAAGGAAGAGCAGGAGATTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGATCCA 900
 DB 841 ACAAGGAAGAGCAGGAGATTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGATCCA 900
 QY 901 AATGTGCTCCAGTGTGAGTGTGCTGCGAGCTCCACCTGCTCCATCTACTCTCATC 960
 DB 901 AATGTGCTCCAGTGTGAGTGTGCTGCGAGCTCCACCTGCTCCATCTACTCTCATC 960
 QY 961 ACACATGATGCGCTATGATTCCTCTACATGATGATGATGAGGACCAATTTGCTC 1020
 DB 961 ACACATGATGCGCTATGATTCCTCTACATGATGATGATGAGGACCAATTTGCTC 1020
 QY 1021 GTGAGCCAGAGCAGGCTGTGAAGTTTCTTTGACATGAGCAAGGGGATGCTCTCTTA 1080
 DB 1021 GTGAGCCAGAGCAGGCTGTGAAGTTTCTTTGACATGAGCAAGGGGATGCTCTCTTA 1080
 QY 1081 CACACACTAGAGCCCTCATCCACAGACATGACATCAATAGCCGTAATGATGAT 1140
 DB 1081 CACACACTAGAGCCCTCATCCACAGACATGACATCAATAGCCGTAATGATGAT 1140
 QY 1141 GAGGACATGACTGCCCAATTAGCATGAGCTGATGCAATTTCTTTTCAATGTCCTGT 1200
 DB 1141 GAGGACATGACTGCCCAATTAGCATGAGCTGATGCAATTTCTTTTCAATGTCCTGT 1200

QY 1201 CGCATGTATGACCTGCTGGTAGCCCCGAAAGCTCTGCAGAGAAAGCCCTGAAGACACA 1260
DB 1201 CGCATGTATGACCTGCTGGTAGCCCCGAAAGCTCTGCAGAGAAAGCCCTGAAGACACA 1260
QY 1261 AACAGAGCCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTCGTGACACGG 1320
DB 1261 AACAGAGCCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTCGTGACACGG 1320
QY 1321 GAGGTACCTTTGCTGACCTCCCAATATGAGATGGAATGAAGGTGGCATTGGAAGGC 1380
DB 1321 GAGGTACCTTTGCTGACCTCCCAATATGAGATGGAATGAAGGTGGCATTGGAAGGC 1380
QY 1381 CTTGGCCCTACCATCCCAAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
DB 1381 CTTGG---TACATCCCAAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1437
QY 1441 ATGAATGAAGACCTTGCAAGCGACCCAAATTTGACATGATGTGCTTATCCTTTGAGAAG 1500
DB 1438 ATGAATGAAGACCTTGCAAGCGACCCAAATTTGACATGATGTGCTTATCCTTTGAGAAG 1497
QY 1501 ATGCAGGACAAGTAGGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTCGGGACATGGT 1560
DB 1498 ATGCAGGACAAGTAGGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTCGGGACATGGT 1557
QY 1561 TGGGGGAATGCACCTCCCAAGCAGCAGGCTCTGTTGCTCTCCCGCCCTCCAGTCAT 1620
DB 1558 TGGGGGAATGCACCTCCCAAGCAGCAGGCTCTGTTGCTCTCCCGCCCTCCAGTCAT 1617
QY 1621 GGTACTACCCAGCCTGGGGTCCATCCCTTCCCGCATCCCTACCATGTGCGCAAGAGG 1680
DB 1618 GGTACTACCCAGCCTGGGGTCCATCCCTTCCCGCATCCCTACCATGTGCGCAAGAGG 1677
QY 1681 GCGGGCTCAGAGCTTCTCACTTCCACATGGTGTCTCCCAACATGGAGGGATCAGCC 1740
DB 1678 GCGGGCTCAGAGCTTCTCACTTCCACATGGTGTCTCCCAACATGGAGGGATCAGCC 1737
QY 1741 CCGCCTGTCAACAATAAGTTTATTATGAAAAAATTTTATGAAAAAATTTTATGAAAAA 1789
DB 1738 CCGCCTGTCAACAATAAGTTTATTATGAAAAAATTTTATGAAAAAATTTTATGAAAAA 1786

RESULT 7

US-08-700-575-35
; Sequence 35, Application US/08700575
; Patent No. 5817479
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Philip R.
; APPLICANT: Wilde, Craig G.
; TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,575
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J
; REGISTRATION NUMBER: 36749
; REFERENCE/DOCKET NUMBER: SP-100 US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Cardiac Muscle
; CLONE: 184416
; US-08-700-575-35

Query Match 7.5%; Score 133.8; DB 1; Length 152;

Best Local Similarity 98.0%; Pred. No. 1e-28; Mismatches 2; Indels 1; Gaps 1;

Matches 146; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 780 GAAGGCGCGCTGGCAGGGCAATGACATTGTCGTGAAGGTGCTGAAGGTTCGAGACTGGAG 839
DB 5 GGAAGGCGCTGGCAGGGCAATGACATTGTCGTGAAGGTGCTGAAGGTTCGAGACTGGAG 64
QY 840 TACAAGGAAGCAGCAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCC 899
DB 65 TACAAGGAAGCAGCAGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCC 123
QY 900 AATGTCTCTCCAGTGTAGTGCCTGCC 928
DB 124 AATGTCTCTCCAGTGTAGTGCCTGCC 152

RESULT 8

US-09-620-312D-95
; Sequence 95, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_files Version 1.0
; SEQ ID NO 95
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (372)..(2894)
; US-09-620-312D-95

Query Match 4.2%; Score 75.4; DB 4; Length 2894;
Best Local Similarity 52.4%; Pred. No. 2.2e-11;
Matches 166; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 269 TGCACGGCCCTGCGGAGGAGGCGCCCTGCTGCTGTGAGATGTTGATCATCGGGGG 328
DB 439 TGCACGGGACACATACATGAGGCGCACTTGATGTTGATGCTCATTTACATGCGG 498
QY 339 CACGATCATGATGTAAGACCGTGGGATGACACCCCTGATCTGGAGAGCATCATG 388
DB 499 CAGAAAGTACCTGTAAAGGATTAAGGCTTATACCCCTGATCTGATGCTGAGCTTCAAG 558
QY 389 GACACCGTATATTTATACAGAACTATTGACATACAGACACATCATCATGATGATG 448
DB 559 GACATATTAATTTGTTCAAGCATCTCTGACCTGGGGTGAATGATGAAATCATG 618
QY 449 AACACGGGAATGSCCCCTGACATATGCTTTTGGGCGCAAGATCAATGAGAGAG 508
DB 619 TCTATGAAATACAGCGCTTACATGCTGCTACATGACAGATGCTGTGTTAAG 678
QY 509 ACCGTGTGCAATGGGCGCTTGTACATCTGTAAAGATGAGAGATGCTGTG 568
DB 679 AGTTATGACTACGCTGTAAAGTAAACAGCAACAAATATGAGTTTACCCCTTTGC 738
QY 569 ACAAGCCAGGACACC 585
DB 739 ATTTGCTGCTGCTCC 755

RESULT 9
US-09-172-977-2
; Sequence 2, Application US/09172977
; Patent No. 5989863
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN ANKRYN FAMILY PROTEIN
; FILE REFERENCE: P-0615 US
; CURRENT APPLICATION NUMBER: US/09/172,977
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1808075
US-09-172-977-2

Query Match 4.0%; Score 71.2; DB 2; Length 1288;
Best Local Similarity 48.3%; Pred. No. 2.3e-10;
Matches 199; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 226 GAGAAAGCATTAACCAAGGAGGAGATCATGCTTCTCCCTTGACTGGGCTGCGCA 285
DB 630 GACAACTCTGTCAACAGCAGACGCGGCTTACCCCTCATCTGGGCTTCCGCG 749
QY 286 GAGGCGCTGCTGTGTTGATGATGATGAGGCGGCGACGATCAATTAATG 345
DB 750 TTTGAGAGATTGAACCGTTCTTCTGCTGAGTGGGGTGGACCCCACTCTG 809
QY 346 AACCGTGGGATGACACCCCTGATCTGGACGACATGACACCGTATATTGA 405
DB 810 GCAAAAGAGGAGAGGCGCTGTGCGGACAGACGCGGCTTACCAACATTTGG 869
QY 406 CAGAAAGCTATTGACATCAAGCAGACATCAATGAGTAAACCGGATGTGCC 465
DB 870 GGGCTGCTGAGACGTTGACCTGACATCAATCTATGATGGAATGAGAGGAGCGCA 929
QY 466 CTGACATATGCTGTTTGGGCGCAAGTCAAGTGGAGAGACTGTGCAATGGG 525

DB 920 CTGCTGTACGCTGTGCGGGAACCACTGAATGCTTTGAGGCTTGCCCGGAGGC 989
QY 526 GCCCTTGCACATCTGTAACAGATGAGAGATGCTGTGAGACAAAGCCAGCACCC 585
DB 990 GCTGACCTTACACACGAAAGCGACTCTGCTACACCCGATGAGACTTGTGCGCTG 1049
QY 586 CTGAGAGACTTCTCGAGAGCGGCGGAGAAAGATGCGCCAGATCTCAACC 637
DB 1050 GGATACCGAAAGTCAACAGGTATGAGAAACCATCTCAAGCTCTTCC 1101

RESULT 10
US-09-702-705-1406
; Sequence 1406, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1406
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1406

Query Match 3.4%; Score 61.6; DB 4; Length 486;
Best Local Similarity 49.7%; Pred. No. 7.5e-08;
Matches 157; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 254 ATGCTTCTCCCTTGTGACTGGGCTTCCGAGAGGCGGCTGTGCTGTGATGATGT 313
DB 166 ATGCTGTACTCCCTTACATTATGCGAGTTGCAAAAACAGCATGAGATCGCTGTCACT 225
QY 314 TGATCATCGGGGCGACGATCAATGTAATGAACCGTGGGATGACACCCCTGCATC 373
DB 226 TACTGAAAGGCGGCTTAATCAAGTCTTAAGACCATTAAGAGCTTACAGCAATGCACC 285
QY 374 TGGCAGCAGTATGACACCGTATATTGTAAGAACTATTGCAAGTATGCAAGGACACA 433
DB 286 GGGCAGCAGCAAGGATTAATTAAGATGATTAATCTTCTGTATCAACAAAGCATCCA 345
QY 434 TCAATGCAATGTAAGAACAGCGGAATGCCCCCTGACATATGCTGTTTGGGCGCAAG 493
DB 346 CAATATCAAGACACTGAGGATTAACCTCTTACACTTACGCTGTATGAGGAGAGAG 405
QY 494 ATCAAGTGGAGAGACTGTGAGCAATGAGGCGCTTGTGACATCTGTAAACAAGTATG 553
DB 406 TGAAGAAAGAAACTGCTGTGTTCCCAAGAGCAAGATTAATTAATTAAGTAAGAG 465
QY 554 GAGAGATGCTGTGGA 569
DB 466 AAAAGACACCCCTGCA 481

RESULT 11
US-09-736-457-1406
; Sequence 1406, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:


```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ; HYPOTHETICAL: NO
; US-09-196-387-1

Query Match 3.4%; Score 61.6; DB 3; Length 4134;
Best Local Similarity 51.1%; Pred.No.2.3e-07;
Matches 145; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy 189 CAACGCAGTCGCCGTTGCGCTGGCGTGGACACACGAGAGACGACTCAACCCAGGGGA 248
    |||||
Db 2087 CAACCCGCTGCTGTTGTAGAGTACCTGCTACACCACGGTCCGATGTCATGCCAAGA 2146
    |||||

Qy 249 CGATCATGGCTTCTCCCGCTTGCACTGGGCTCCGAGAGGGCGCTCTGCTGTGGTTGA 308
    |||||
Db 2147 CAAGGGTGGCTTGGTGCCCCCTTCATATGCTCTTCATATGACACATATGAGGTGGCTGA 2206
    |||||

Qy 309 GATGTTTCATCATCGGGGGGCACGGATCAATGTAATGAACCGTGGGGATGACACCCCT 368
    |||||
Db 2207 GCTTTTAGTAAAGCATGGGGCTTCTGTAATGGCGGACTTATGAAATTTTACCCCTCT 2266
    |||||

Qy 369 GCATCTGGCAGCCAGTCATGGACACCGCTGATATGTTACAGAAGCTATTGCAGTACAAGGC 428
    |||||
Db 2267 CCATGAAGCAGCAGCTAAGGAAGTATGAAATCTGCAAGCTCTTTTAAACATGGAGC 2326
    |||||

Qy 429 AGACATCAATGCAGTGAATGAACACCGGAATGTCCTCGACT 472
    |||||
Db 2327 AGATCCAACTAAAAAGAACAGACATGGAATACACCTTTGGATT 2370
    |||||

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```

RESULT 13
US-09-841-835-1
; Sequence 1, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30

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Query Match	3.4%;	Score 61.6;	DB 4;	Length 4134;
Best Local Similarity	51.1%;	Pred. No. 2.3e-07;		
Matches 145;	Conservative	0;	Mismatches 139;	Indels 0

RESULT 14
US-09-196-387-7

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? Sequence', Application US/09196387
? Patent No. 6277613
?
? GENERAL INFORMATION:
?
? APPLICANT: de Lange, Tilia
? APPLICANT: Smith, Susan
? TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
? TITLE OF INVENTION: OF USE THEREOF
? NUMBER OF SEQUENCES: 12
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Klauber & Jackson
? STREET: 411 Hackensack Avenue, 4th Floor
? CITY: Hackensack
? STATE: New Jersey
? COUNTRY: USA
?
? ZIP: 07601
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: FLOPPY disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:

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LOCATION: 6..2027
US-09-196-387-7

RESULT 15
US-09-841-835-7

```

: Sequence #, Application US/09841835
: Patent No. 6506587
:
: GENERAL INFORMATION:
:
: APPLICANT: de Lange, Titia
: APPLICANT: Smith, Susan
: TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
: TITLE OF INVENTION: OF USE THEREOF
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSES: Klauber & Jackson
: STREET: 411 Hackensack Avenue, 4th Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
:

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D_b 61 CCCGAGGATAAAGC


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QY 1183 TCTTCCCAATGTCCTGGTCGATGTATGCACTGCTGGGTAGCCCCGAAAGCTCTGCAG 1242
Db 404 TCTTTCCAAATGTCCTGGTCGATGTATGCACTGCTGGGTAGCCCCGAAAGCTCTGCAG 463
QY 1243 AAGAAGCCTGAAGACACAAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTGTCTTG 1302
Db 464 AAGAAGCCTGAAGACACAAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTGTCTTG 523
QY 1303 TGGGAACCTGGTCACACGGGAGGTACCTTTGCTGACCTCTCCAATATGGAGATTGGAAATG 1362
Db 524 TGGGAACCTGGTCACACGGGAGGTACCTTTGCTGACCTCTCCAATATGGAGATTGGAAATG 583
QY 1363 AAGGTGGCATTTGGAAGGCTTCGGGCTTACCATCCCAACAGGTATTTCCCTCATGTGTGT 1422
Db 584 AAGGTGGCATTTGGAAGGCTTCGGGCTTACCATCCCAACAGGTATTTCCCTCATGTGTGT 643
QY 1423 AAGCTCATGAAGATCTGCATGAATGAAGACCTCGAAGCGACCCAAATTTGACATGATT 703
Db 644 AAGCTCATGAAGATCTGCATGAATGAAGACCTCGAAGCGACCCAAATTTGACATGATT 703
QY 1483 GTGCTATCTTGAAGATCGAGACAAAGTAGGACTGGAAGGTCCTTGCCTGAACCTCA 1542
Db 704 GTGCTATCTTGAAGATCGAGACAAAGTAGGACTGGAAGGTCCTTGCCTGAACCTCA 763
QY 1543 GAGGTGTCGGGACATGTTGGGGGAATGCACCTCTCCCAAGCAGCAGGCTCTGTTGCC 1602
Db 764 GAGGTGTCGGGACATGTTGGGGGAATGCACCTCTCCCAAGCAGCAGGCTCTGTTGCC 823
QY 1603 TCCCGCGCTCCAGTCATGTTACTACCCAGCC-TGGGGTCATCCCTTCCCGCATCC 1661
Db 824 TCCCGCGCTCCAGTCATGTTACTACCCAGCCATGGGTCATCCCTTCCCGCATCC 883
QY 1662 TACCACCTGTG--CGCAAGAGGGGGGCTCAGAGCTTGTCACTTGCACATGTTGCTC 1719
Db 884 TACCACCTGTGCCCCAAGAGGGGGGCTCAGAGCTTGTCACTTGCACATGTTGCTC 943
QY 1720 CCAACATGGGAGGATCAGCCCGCTCTCAATAAAAGTTTAT 1763
Db 944 CCAACATGGGAGGATCAGCCCGCTCTCAATAAAAGTTTCT 987

RESULT 4
US-09-918-995-15193
; Sequence 15193, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15193
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(484)
; OTHER INFORMATION: n = A,T,C or G
Query Match 24.4%; Score 437.4; DB 11; Length 484;
Best Local Similarity 99.5%; Pred. No. 4.9e-127;
Matches 438; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 952 ACTCTCATCACACTGGATCGGTATGGATCCCTCTCAATATGTAATGAAGGCACC 1011
Db 44 ACNCTCATCACACTGGATCGGTATGGATCCCTCTCAATATGTAATGAAGGCACC 103
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QY 1012 AATTTCTGTCGTGGACCAAGCGCTGTGAAGTTTCTTGGACATGGCAAGGGCATG 1071
Db 104 AATTTCTGTCGTGGACCAAGCGCTGTGAAGTTTCTTGGACATGGCAAGGGCATG 163
QY 1072 GCCTTCTTACACACATAGAGCCCCCTCATCCACGACATGCACCTCAATAGCCGTAGTGT 1131
Db 164 GCCTTCTTACACACATAGAGCCCCCTCATCCACGACATGCACCTCAATAGCCGTAGTGT 223
QY 1132 ATGATTGATGAGGACATGACTGCCCGAATTAGCATGCTGATGTCAGTTCTCTTTCCAA 1191
Db 224 ATGATTGATGAGGACATGACTGCCCGAATTAGCATGCTGATGTCAGTTCTCTTTCCAA 283
QY 1192 TGTCTCTGTCGATGTATGCACTGCTGGGTAGCCCGAAGCTCTGCAAGAAAGCCT 1251
Db 284 TGTCTCTGTCGATGTATGCACTGCTGGGTAGCCCGAAGCTCTGCAAGAAAGCCT 343
QY 1252 GAAGACACAAACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTG 1311
Db 344 GAAGACACAAACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTG 403
QY 1312 GTGACACGGGAGGTACCTTTGCTGACCTCTCCAAATATGAGATTGGAATGAAGGTGCA 1371
Db 404 GTGACACGGGAGGTACCTTTGCTGACCTCTCCAAATATGAGATTGGAATGAAGGTGCA 463
QY 1372 TTGGAAGGCTTTCGGCCCTAC 1391
Db 464 TTGGAAGGCTTTCGGCCCTAC 483

RESULT 5
US-09-918-995-23944
; Sequence 23944, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23944
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(464)
; OTHER INFORMATION: n = A,T,C or G
Query Match 23.9%; Score 427.6; DB 11; Length 464;
Best Local Similarity 99.1%; Pred. No. 5.9e-124;
Matches 430; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 704 ACAAACACTCTGGCATTTGACTTCAAAACAGCTTAACTTCTCAGCAAGCTCAACGAAATC 763
Db 31 AGATACTACTTGGCATTTGACTTCAAAACAGCTTAACTTCTCAGCAAGCTCAACGAAATC 90
QY 764 ACTCTGGAGAGCTATGGAAGGGCCGCTGGCAGGGCAATGACATTTGCTGAAGGTGCTGA 823
Db 91 ACTCTGGAGAGCTATGGAAGGGCCGCTGGCAGGGCAATGACATTTGCTGAAGGTGCTGA 150
QY 824 AGGTTCCGAGACTGGAGTACAAAGGAGACGAGGACTTCAATGAAGAGTGTCCCGGCTCA 883
Db 151 AGGTTCCGAGACTGGAGTACAAAGGAGACGAGGACTTCAATGAAGAGTGTCCCGGCTCA 210
QY 884 GGATTTTCTCGCATCCAAATGTGCTCCAGTGTAGGTGCTGCAAGTCTCCACTGCTC 943
Db 211 GGATTTTCTCGCATCCAAATGTGCTCCAGTGTAGGTGCTGCAAGTCTCCACTGCTC 270
QY 944 CTCACTCTCTCTCATCACACACTGGATGCGGTATGGATCCCTCTCAATATGTAATGATG 1003
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Db 271 CTCATCTACTCTCATCACACAGTCCGATGATCCCTCTACATGACTACATG 330
Qy 1004 AAGGACCAATTTCTCGGACCGAGCCGCTGTGAAGTTTCTTGACATGGCA 1063
Db 331 AAGGACCAATTTCTCGGACCGAGCCGCTGTGAAGTTTCTTGACATGGCA 390
Qy 1064 GGGGCGATGCGCTTCTTACACACATAGAGCCCTCATCCACGATGCAATAGCC 1123
Db 391 GGGGCGATGCGCTTCTTACACACATAGAGCCCTCATCCACGATGCAATAGCC 450
Qy 1124 GTAGTGAATGATT 1137
Db 451 GTAGTGAATGATT 464

RESULT 6
US-09-922-217-435/c
; Sequence 435, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 435
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-435

Query Match 18.4%; Score 328.4; DB 9; Length 330;
Best Local Similarity 99.7%; Pred. No. 8-93;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 996 ACTACATGAAGGACCAATTTCTGCTGACCAAGCCGCTGTGAAGTTTGGTGA 1055
Db 330 ACTACATGAAGGACCAATTTCTGCTGACCAAGCCGCTGTGAAGTTTGGTGA 271
Qy 1056 CATGCAAGGGGCGATGCGCTTCTTACACACATAGAGCCCTCATCCACGATGCACT 1115
Db 270 CATGCAAGGGGCGATGCGCTTCTTACACACATAGAGCCCTCATCCACGATGCACT 211
Qy 1116 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCGCCGAATTAAGCATGATGT 1175
Db 210 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCGCCGAATTAAGCATGATGT 151
Qy 1176 CAAGTTCTCTTCCAAATGCTCGTGTCGATGATGACATCTGCTGCGTGAAGCCCGGAAGC 1235
Db 150 CAAGTTCTCTTCCAAATGCTCGTGTCGATGATGACATCTGCTGCGTGAAGCCCGGAAGC 91
Qy 1236 TCTGCAAGAAAGCTGAAAGACAAACAGAGCTCAGACAGATGTGGAGTTTGCAGT 1295
Db 90 TCTGCAAGAAAGCTGAAAGACAAACAGAGCTCAGACAGATGTGGAGTTTGCAGT 31
Qy 1296 GCTTCTGTGGAACTGTGACACGGGAGGT 1325
Db 30 GCTTCTGTGGAACTGTGACACGGGAGGT 1

RESULT 7
US-09-833-263-435/c
; Sequence 435, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 435
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-263-435

Query Match 18.4%; Score 328.4; DB 10; Length 330;
Best Local Similarity 99.7%; Pred. No. 8-93;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 996 ACTACATGAAGGACCAATTTCTGCTGACCAAGCCGCTGTGAAGTTTGGTGA 1055
Db 330 ACTACATGAAGGACCAATTTCTGCTGACCAAGCCGCTGTGAAGTTTGGTGA 271
Qy 1056 CATGCAAGGGGCGATGCGCTTCTTACACACATAGAGCCCTCATCCACGATGCACT 1115
Db 270 CATGCAAGGGGCGATGCGCTTCTTACACACATAGAGCCCTCATCCACGATGCACT 211
Qy 1116 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCGCCGAATTAAGCATGATGT 1175
Db 210 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCGCCGAATTAAGCATGATGT 151
Qy 1176 CAAGTTCTCTTCCAAATGCTCGTGTCGATGATGACATCTGCTGCGTGAAGCCCGGAAGC 1235
Db 150 CAAGTTCTCTTCCAAATGCTCGTGTCGATGATGACATCTGCTGCGTGAAGCCCGGAAGC 91
Qy 1236 TCTGCAAGAAAGCTGAAAGACAAACAGAGCTCAGACAGATGTGGAGTTTGCAGT 1295
Db 90 TCTGCAAGAAAGCTGAAAGACAAACAGAGCTCAGACAGATGTGGAGTTTGCAGT 31
Qy 1296 GCTTCTGTGGAACTGTGACACGGGAGGT 1325
Db 30 GCTTCTGTGGAACTGTGACACGGGAGGT 1

RESULT 8
US-10-025-380-435/c
; Sequence 435, Application US/10025380
; Patent No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedrick Thomas S.
; APPLICANT: Carter, Darick

;; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;; FILE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

;; CURRENT APPLICATION NUMBER: US/10/025,380

;; CURRENT FILING DATE: 2001-12-19

;; NUMBER OF SEQ ID NOS: 1129

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 435

;; LENGTH: 330

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-10-025-380-435

Query Match 18.4%; Score 328.4; DB 13; Length 330;

Best Local Similarity 99.7%; Pred. No. 8.8e-93; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 1;

QY 996 ACTACATGAAGGCACCAATTTTCGTGGACAGAGCCAGGCTGTGAAGTTTGCTTTGGA 1055

DB 330 ACTACATGAAGGCACCAATTTTCGTGGACAGAGCCAGGCTGTGAAGTTTGCTTTGGA 271

QY 1056 CATGCCAAGGGCATGGCTTCCTACACACTAGAGCCCTCATCCACGACATGCACT 1115

DB 270 CATGCCAAGGGCATGGCTTCCTACACACTAGAGCCCTCATCCACGACATGCACT 211

QY 1116 CAATAGCCGTAGTGTAAATGATTGATGAGGACATGATCGCCGAATTAGCATGGCTGATGT 1175

DB 210 CAATAGCCGTAGTGTAAATGATTGATGAGGACATGATCGCCGAATTAGCATGGCTGATGT 151

QY 1176 CAAGTTCTCTTTCCAAATCTCTGTGCGCATGTATGTCACCTGCTGGGTAGCCCGGAAGC 1235

DB 150 CAAGTTCTCTTTCCAAATCTCTGTGCGCATGTATGTCACCTGCTGGGTAGCCCGGAAGC 91

QY 1236 TCTGCAGAAAGCCTGGAAGACACAAACAGAGCGCTCAGCAGACATGTGGAGTTTGCACT 1295

DB 90 TCTGCAGAAAGCCTGGAAGACACAAACAGAGCGCTCAGCAGACATGTGGAGTTTGCACT 31

QY 1296 GCTTCTGTGGAACTGGTGACACGGGAGGT 1325

DB 30 GCTTCTGTGGAACTGGTGACACGGGAGGT 1

RESULT 9

US-10-106-698-2638

;; Sequence 2638, Application US/10106698

;; Publication No. US20030109690A1

;; GENERAL INFORMATION:

;; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

;; APPLICANT: Ruben et al.

;; FILE REFERENCE: PA005P1

;; CURRENT APPLICATION NUMBER: US/10/106,698

;; CURRENT FILING DATE: 2002-03-27

;; PRIOR APPLICATION NUMBER: PCT/US00/26524

;; PRIOR FILING DATE: 2000-09-28

;; PRIOR APPLICATION NUMBER: US 60/157,137

;; PRIOR FILING DATE: 1999-09-29

;; PRIOR APPLICATION NUMBER: US 60/163,280

;; PRIOR FILING DATE: 1999-11-03

;; NUMBER OF SEQ ID NOS: 8564

;; SOFTWARE: PatentIn Ver. 3.0

;; SEQ ID NO 2638

;; LENGTH: 568

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: (341)..(341)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (395)..(395)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (407)..(407)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (429)..(429)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (444)..(444)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (455)..(455)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (457)..(457)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (508)..(508)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (524)..(524)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (528)..(528)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (555)..(555)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc feature

;; LOCATION: (557)..(557)

;; OTHER INFORMATION: n equals a,t,g, or c

US-10-106-698-2638

Query Match 13.5%; Score 240.8; DB 14; Length 568;

Best Local Similarity 97.2%; Pred. No. 4.6e-65;

Matches 245; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 451 CACGGGAATGTCCTGTCACATGTCCTGTTTGGGCCCAAGATCAAGTGGCAGAGGAC 510

DB 2 CACGGGAATGTCCTGTCACATGTCCTGTTTGGGCCCAAGATCAAGTGGCAGAGGAC 61

QY 511 CTGGTGGCAATGGGGCCCTGTGAGGATCTGTACAGTATGAGAGATGCTGTGGAC 570

DB 62 CTGGTGGCAATGGGGCCCTGTGAGGATCTGTACAGTATGAGAGATGCTGTGGAC 121

QY 571 AAAGCCAAGGCACCCCTGAGAGAGCTTCTCCAGAGCGGGCAGAGAAAGATGGCCAGAAAT 630

DB 122 AAAGCCAAGGCACCCCTGAGAGAGCTTCTCCAGAGCGGGCAGAGAAAGATGGCCAGAAAT 181

QY 631 CTCAACCGTATTCATACAAAGGACACATTTCTGGAAGGGGACACCCCGCCTCGGCCCGGA 690

DB 182 CTCAACCGTATTCATACAAAGGACACATTTCTGGAAGGGGACACCCCGCCTCGGCCCGGT 241

QY 691 AATGGAACCTGTG 702

DB 242 GAGTCACCACTG 253

RESULT 10

US-09-814-353-14739

;; Sequence 14739, Application US/09814353

;; Publication No. US20030165831A1

;; GENERAL INFORMATION:

;; APPLICANT: Lee, John

;; APPLICANT: Thompson, Pamela

;; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

;; FILE REFERENCE: MRI-006B

;; CURRENT APPLICATION NUMBER: US/09/814,353

;; CURRENT FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: US 60/191,031

;; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: US 60/207,124

;; PRIOR FILING DATE: 2000-05-25


```

; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14739
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-14739

Query Match      9.5%; Score 170.2; DB 12; Length 506;
Best Local Similarity 98.3%; Pred. No. 7.5e-43;
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1123 CGTACTGTAATGATGAGACATGACTGCCCGAATTAGCATGCTGATGTCAGTTTC 1182
DB      332 CGTCGGTAATGATGAGACATGACTGCCCGAATTAGCATGCTGATGTCAGTTTC 391

QY      1183 TCTTCAATGCTCGTGCATGTATGACCTGCTGGGTAGCCCCGAACTCTGCAG 1242
DB      392 TCTTCAATGCTCGTGCATGTATGACCTGCTGGGTAGCCCCGAACTCTGCAG 451

QY      1243 AAGAAGCTGAAGACAAACAGAGCTCAGACATGTGAGTTTTCAGACTGC 1297
DB      452 AAGAAGCTGAAGACAAACAGAGCTCAGACATGTGAGTTTTCAGACTGC 506

RESULT 11
US-09-917-800A-187/C
; Sequence 187, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Casle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 187
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA866435
US-09-917-800A-187

Query Match      7.1%; Score 127.8; DB 10; Length 301;
Best Local Similarity 70.8%; Pred. No. 1.3e-29;
Matches 213; Conservative 0; Mismatches 82; Indels 6; Gaps 3;

QY      1493 TTGAGAAATGCAGACAAAGTAGAGCTGGAAGTCTGCTGAACTCCAGAGGTGG 1552
DB      301 TCGAGAAATGCAGACAAAGTAGAGCTGGAAGTCTGCTGAACTCCAGAGGTGG 242

QY      1553 GACATGTTGGGGGAATGCACCTCCCAAGACAGAGCCTCTGTTGCTCCCGGCT 1612
DB      241 CATATGCTGAGACGAATTAATTTCCCTGAAGTGAAGATTGTGCTGCTCCAGTCT 182

QY      1613 CCAGTCATGTAATACCCGAG-CTGGGGTCCATCCCTTCCCATCCTAACACTGT- 1670
DB      181 CTAAATCGGTGTAATACCCAGACAGCGGAGACTTCCCTGTGCATCATCAACACTGTA 122

QY      1671 --GCCAGAGGGGGGCTCAGAGCTTGTCACTTGCACATGGTGTCT--TCCAGACT 1726
DB      121 GCCCTGAGAGACATGGGCACAGACAGACTGTCAATGCAATGATTCACAGACT 62

QY      1727 GGGAGGATCAGCCCCGCTGTCAACATTAAGTTTATGAAAAAATTTTATGAAAAA 1786
DB      61 GGGAGGATCAGCACTGCTGTAAACATTAATAGTGGAAAAAATTTTATGAAAAA 2

QY      1787 A 1787
DB      1 A 1

RESULT 12
US-09-814-353-2009
; Sequence 2009, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2009
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-2009

Query Match      6.9%; Score 123.2; DB 12; Length 462;
Best Local Similarity 97.7%; Pred. No. 4.6e-28;
Matches 125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1123 CGTAGTGAATGATTGATGAGACATGACTGCCGAATTAGCATGGCTGATGTCGAAGTTC 1182
Db 335 CGTCGGGTAATGATTGATGAGACATGACTGCCGAATTAGCATGGCTGATGTCGAAGTTC 394
QY 1183 TCTTTCCAAATGCTCTGGTCGCGATGATGCACCTGCTGGTAGCCCGAAGCTCTGCAG 1242
Db 395 TCTTTCCAAATGCTCTGGTCGCGATGATGCACCTGCTGGTAGCCCGAAGCTCTGCAG 454
QY 1243 AAGAAGCC 1250
Db 455 AAGAAGCC 462

RESULT 13

US-09-814-353-8355
; Sequence 8355, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8355
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8
; OTHER INFORMATION: n = A,T,C or G

Query Match 6.9%; Score 123.2; DB 12; Length 462;
Best Local Similarity 97.7%; Pred. No. 4.6e-28;
Matches 125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1123 CGTAGTGAATGATTGATGAGACATGACTGCCGAATTAGCATGGCTGATGTCGAAGTTC 1182
Db 335 CGTCGGGTAATGATTGATGAGACATGACTGCCGAATTAGCATGGCTGATGTCGAAGTTC 394
QY 1183 TCTTTCCAAATGCTCTGGTCGCGATGATGCACCTGCTGGTAGCCCGAAGCTCTGCAG 1242
Db 395 TCTTTCCAAATGCTCTGGTCGCGATGATGCACCTGCTGGTAGCCCGAAGCTCTGCAG 454
QY 1243 AAGAAGCC 1250
Db 455 AAGAAGCC 462

RESULT 14

US-09-783-590-2528
; Sequence 2528, Application US/09783590
; Patent No. US20020110850A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIORITY FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2528
; LENGTH: 197
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (27)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (33)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (39)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (46)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (63)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (118)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (133)
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; NAME/KEY: misc_feature
; LOCATION: (155)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (177)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (188)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (194)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-783-590-2528

Query Match 5.0%; Score 89; DB 10; Length 197;
Best Local Similarity 83.2%; Pred. No. 1.8e-17;
Matches 153; Conservative 0; Mismatches 26; Indels 5; Gaps 5;

QY 52 AGCCCGAGTCCGAGGATAAAGCTTGGGTTTCATCTCTCTCCCTTGG-ATCACTCCACAG 110
Db 6 ACCCAAAGTCCGAGGATAAANCTTGGNGTTAAANCTCTCTCCCTTGGAAATCACTCCANAG 65

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REFERENCE	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Tateyama,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsch,G., Blake,J., Brownstein,M.J., Bult,C., Carninci,P., de Bonaldo,M.P., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wyshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217551
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1728)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000)
COMMENT	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATTCGAGATCTTAAATTAATCCCCCCCCC 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase

Oy 702 GAACAACAACCTGCGCATTTGACCTTCAAAACAGCTTAATCTTGACGAAAGCTCAACGAGAA 761
 Db 659 GAACAACAACCTGCGCATTTGACCTTCAAAACAGCTTAATCTTGACGAAAGCTCAACGAGAA 718
 Oy 762 TCACTCTGAGAGCATGAGAAAGGCGCTGGCAGGGCAATGACATTTGCTGAGAGTGTCT 821
 Db 719 TCATTCTGAGAGCTTTGAAAGGCGCTGGCAGGGCAATGATTTGTTGTAAGTGTCT 778
 Oy 822 GAAGTTTGAGCATCTGAGATACAGAGAGAGAGGAGCTTCAATGAAGAGTGTCTCCCGGT 881
 Db 779 GAAGTTTGAGCATCTGAGATACAGAGAGAGAGGAGCTTCAATGAAGAGTGTCTCCCGGT 838
 Oy 882 CAGATTTTCTGCGCATTTGCTGCTCCAGTGTAGAGTGTCTCCAGTGTCTCCAGTGTCT 941
 Db 839 CAGATTTTCTGCGCATTTGCTGCTCCAGTGTAGAGTGTCTCCAGTGTCTCCAGTGTCT 898
 Oy 942 TCTTCATCTTACTCTGATCAGACACTGTGATGATGATGATGATGATGATGATGATGATGAT 1001
 Db 899 CCCCCCAACCTCATCAGACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
 Oy 1002 TGAAGGCAACCAATTTCTGCTGCTGAGACAGAGCTGTGAAGTTGCTTTGAGACATGCTG 1061
 Db 959 TGAAGGCAACCAATTTCTGCTGCTGAGACAGAGCTGTGAAGTTGCTTTGAGACATGCTG 1018
 Oy 1062 AAGGGGCAATGCTTCTTACACACACTGAGAGCTTCAATCCAGACATGACATGACATGAC 1121
 Db 1019 AAGGGGCAATGCTTCTTACACACACTGAGAGCTTCAATCCAGACATGACATGACATGAC 1078
 Oy 1122 CCGTAGTGAATGATTTGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1181
 Db 1079 CCGTAGTGAATGATTTGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
 Oy 1182 CTCTTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
 Db 1139 TTTCTTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1198
 Oy 1242 GAAGAAGCTGTAAGACACAAACAGAGCTGACAGACATGATGATGATGATGATGATGATGAT 1301
 Db 1199 GAAGAAGCTGTAAGACACAAACAGAGCTGACAGACATGATGATGATGATGATGATGATGAT 1258
 Oy 1302 GTGGGAACTGTGATGACACGAGAGTACCTTTGCTGACCTTCCAAATGATGATGATGATGAT 1361
 Db 1259 GTGGGAACTGTGATGACACGAGAGTACCTTTGCTGACCTTCCAAATGATGATGATGATGAT 1318
 Oy 1362 GAAGTGTGATGAGAGGCTTGGGCTTACCAATGATGATGATGATGATGATGATGATGATGAT 1421
 Db 1319 GAAGTGTGATGAGAGGCTTGGGCTTACCAATGATGATGATGATGATGATGATGATGATGAT 1378
 Oy 1422 TAAGTGTGATGAGAGTGTGATGAGAGGCTTGGGCTTACCAATGATGATGATGATGATGAT 1481
 Db 1379 TAAGTGTGATGAGAGTGTGATGAGAGGCTTGGGCTTACCAATGATGATGATGATGATGAT 1438
 Oy 1482 TGTGCTTATCTTGTGAGAGATGACAGACATGATGATGATGATGATGATGATGATGATGATGAT 1541
 Db 1439 TGTGCTTATCTTGTGAGAGATGACAGACATGATGATGATGATGATGATGATGATGATGATGAT 1498
 Oy 1542 AGAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1601
 Db 1499 AGAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
 Oy 1602 CTCCCCCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1660
 Db 1559 CTCCCCCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1618
 Oy 1661 CTACCATGCT--GGCAAGAGAGGCGGCTCAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1717
 Db 1619 CTACCATGCTGAGCCCAAAAGAGGCGGCTCAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1678
 Oy 1718 TCCCAACATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1766
 Db 1679 TCCCAACATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1727

RESULT 2
 AK002344
 LOCUS
 DEFINITION
 Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:061008K16 product:integrin linked kinase, full insert sequence.
 ACCESSION
 AK002344
 VERSION
 AK002344.1 GI:12832253
 KEYWORDS
 HTC, CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 2 99279253
 10349636
 REFERENCE
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 REFERENCE
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, Y., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohtsuka, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, T., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 REFERENCE
 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fletschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stanbly, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Baren, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombereis, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, S., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whiteaker, C., Wilming, L., Wyshew-Borie, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohetsuki, S. and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 21085660
 11217851
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1705)
 REFERENCE
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno,M., Hanagaki,T., Hata,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGGATCCAGAGCTCAATTAAATTAACCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES

source

Location/Qualifiers
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BASE COUNT 412 a 455 c 459 g 378 t 1 others

ORIGIN

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 Matches 1496; Conservative 0; Mismatches 167; Indels 7; Gaps 4;
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 DB 279 GATGAATCGTGGGATGATACCCCTGCACTGGCAGCTAGTATGACACACCGTGAT 338
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 QY 462 GCCCTGCACATCTGCTGTTTTCGGGCGCAAGATCAAGTGGCAGGACCTGTGGGCAAA 521
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Db	1536	CTCCCCGTCTCTAATCATGTGTACTATCCCAAGTTATGGGACTTGTTCCTCTCCATCC	1595
OY	1661	CTACCACTGT--GCGCAAGAGGGGCGGGCTCAGAGCTTTGTCACTTGCCACATGATGTC	1717
Db	1596	CTACCACTGTAGCCCCCAAAAGGGGCTGGGGCTCAGAGCTTTGTCACTTGCCACATGATGTC	1655
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RESULT 3	AL579747/c	LOCUS	DEFINITION
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	AL579747	Homo sapiens T	CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
	Homo sapiens cdna	CDS0D003YX18	3-PRIME, mRNA sequence.

VERSION	AL579747.2	GI:31316027
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 base(s) from 1 to 1201
 Li, W.B., Gruber, C., Jesssee, J. and Polayes, P.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 16, 2001 this sequence version replaced gi:12945092.

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segrete@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ003BF09NP1&cluster=6100.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DJ003BF09NP1&cluster=6100.f). Contact :
Feng liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Faraday Avenue Genoscope sequence ID : CS0DJ003BF09NP1.

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Matches 1067; Conservative	30; Mismatches 44; Indels 9; Gaps 7;

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ACCESSION AL528727
VERSION AL528727.2 GI:31066577
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12792220.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD001BF09QPl&cluster=6100.f. Contact :
Feng Liang, Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD001BF09QPl.
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Matches 1048; Conservative 17; Mismatches 49; Indels 14; Gaps 4;

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Db 425 GTGACACAGAGCCAGGCTGTGAAGTTTGTGACATGGAAGGGGATGGCTTCTCTA 484

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LOCUS AL579748 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DJ003YK18 5-PRIME, mRNA sequence.
ACCESSION AL579748
VERSION AL579748.2 GI:31318028

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12945094.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D003BF09P1&cluster=6100.f. Contact :
Peng Liang Email : filiang@life.techn.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
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10-NORMALIZED"
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 295 a 303 c 319 g 245 t 39 others
ORIGIN

Query Match 54.1%; Score 968.6; DB 9; Length 1201;
Best Local Similarity 98.4%; Pred. No. 1.1e-136;
Matches 1005; Conservative 4; Mismatches 8; Indels 4; Gaps 3;

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QY 395 GTGATATTGTACAGAACTATTGAGTCAAGGAGAGATCAATGAGATGAAACAG 454
DB 382 GTGATATTGTACAGAACTATTGAGTCAAGGAGAGATCAATGAGATGAAACAG 441
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DB 442 GGAATGTGCCCCGTGACTATGCTGTTTGGGGCCAAGATCAAGTGCAGAGACTGG 501
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LOCUS AL528726 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0D001YK18 3-PRIME, mRNA sequence.
ACCESSION AL528726
VERSION AL528726.2 GI:31066576
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12792219.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D001BF09NP1&cluster=6100.f. Contact :
Peng Liang Email : filiang@life.techn.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D001BF09NP1.
Location/Qualifiers

FEATURES


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DEFINITION CDNA clone CS0DC017YH20 3-PRIME, mRNA sequence.
ACCESSION BX332970
VERSION BX332970.1 GI:30310200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li W.B., Gruber,C., Jessee,J. and Pollayes,D.
Unpublished
Full-length cDNA libraries and normalization
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC017DD10NP1&cluster=6100.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC017DD10NP1.
Location/Qualifiers
1..1200
FEATURES
source
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/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 261 a 286 c 317 g 286 t 50 others
ORIGIN
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Best Local Similarity 95.9%; Pred. No. 4.5e-12;
Matches 1009; Conservative 16; Mismatches 17; Indels 10; Gaps 6;
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Db 450 GCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTGTTGTTGACACGCGGAGGTACCCCTT 391
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Db 390 GCTGACCTCTCCAATATGAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 333
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Db 332 ATCCCAACAGGTATTTCCCTCATGTGTGAAGCTCATGAAGATCTGCAATGAATGAAGAC 273
Qy 1453 CTGCAAGAGCAGCCAAATTTGACATGATTTGCTGCTATCTTCTTGAAGAGATGAGAGCAAG 1512
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QY	1573	CCTCCCAAGAGCAGCAGGCTCTGGTTGCTCCCGGCTCCAGTCATGTAATACCCCA	1632
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QY	1633	GCC-TGGGGTCATCCCTTCCCGCATCCCTACCACTGTG--CGCAAGAGGGCGGGCTC	1688
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QY	1690	AGAGCTTGTCACTTGCACATGGTGTCTCC	1721
Db	32	AGAGCTTGTCACTTGCACATGGTGTCTCC	1
RESULT 10	AL569057/c		
LOCUS	AL569057	1201 bp	mRNA linear EST 13-MAY-2003
DEFINITION	AL569057 Homo sapiens PLACENTA	Homo sapiens cDNA clone CS0DE003D17	
ACCESSION	AL569057		
VERSION	AL569057.2	GI:30605114	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12924017.		

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email : segr@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f. For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDBE003CB9NP1&cluster=6100.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSDBE003CB9NP1&cluster=6100.f). Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CSDBE003CB9NP1.
Location/Qualifiers
1..1201

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/organism="Homo sapiens"
/mol_type="mRNA"
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/vector="PCMVSPORT 6: 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the PCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      245 a      296 c      323 g      296 t      41 others
ORIGIN

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Query Match	52.3%	Score 935	DB 9	Length 1201
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QY	709	CACCTGGCATTAAGCTTCAACACAGCTTAACCTCTGACGAAAGCTCAAGAGATCACTCT	768	
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OY	769	GGAGAGCTATGGAAGGCCCGCTGGCAGGGCAATGACATTGTGCTGTAAGTCTGAAGTT	828
Db	971	GGAAGACTATGAAAGGGCCGCTGGCAGGGCAATATCATTTGTGTGAAGTCTGAAGTT	912
OY	829	CGAGACTGGAATACAAGAAGAGAGGAACTTCATGAAAGATGTCCCGGCTCAGATTT	888
Db	911	CGAARCTGGAGAACAGGAAGAGAGGAACTTCATGAAAGATGTCCCCGGCTCAGATTT	852
OY	889	TTCTTGCAATCCAATATGTCTCCAGTGTAGTGCCTGCACTCCAGTCTCCACTGCTTCAT	948
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Db	791	CCTACTCTGCATCACACACTGGAATGCCGTAATGATTCCTCTCAAATGTAATAAGAGC	732
OY	1009	ACCAATTTTCGTGTGAGCACAGAGCCAGGCTGTGAAGTTTGCTTGGACATGGCAAGGGC	1068
Db	731	ACCAATTTTCGTGTGAGCACAGAGCCAGGCTGTGAAGTTTGCTTGGACATGGCAAGGGC	672
OY	1069	ATGGCTTTCCTACACACCTAGAGCCCTCATTCOAGACATGCACTCAATAGCCCTAGT	1128
Db	671	ATGGCTTTCCTACACACCTAGAGCCCTCATTCOAGACATGCACTCAATAGCCCTAGT	612
OY	1129	GTAATGATGTAATGAGACATAGACTGCCCAGATTATGACATGGCTGATGTCAAGTTCCTTC	1188
Db	611	GTAATGATGTAATGAGACATAGACTGCCCAGATTATGACATGGCTGATGTCAAGTTCCTTC	552
OY	1189	CAATGTCCCTGTGTGCATGTATGACACTGTGCGGTAGGCCCCGAAAGCTCTGCAGAAAG	1248
Db	551	CAATGTCCCTGTGTGCATGTATGACACTGTGCGGTAGGCCCCGAAAGCTCTGCAGAAAG	492
OY	1249	CCTGAAGACAAACAGACGCTCAGACAGACATGTGGAGTTTTCAGAGTCTCTGTGGAA	1308
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OY	1309	CTGTGACACAGGAGGTACCCTTGTGTGACCTCTCAATATGAGATTTGAATGAAGSTG	1368
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OY	1668	TGTG -- CGCAAGAGGGGGGCTGAGACTTTGTCACTTGGCACATGATGTCTCCCAACA	1729
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ALU55417			
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DEFINITION	CDNA clone CS0DK008Y0L4 5-PRIME, mRNA sequence.		
ACCESSION	ALU55417		
VERSION	ALU55417.2	GI:31277224	

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KEYWORDS      EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE         1 (bases 1 to 994)
JOURNAL       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
              Full-length cDNA libraries and normalization
              Unpublished
COMMENT       On Feb 15, 2001 this sequence version replaced gi:12897130.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 6100.f For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0DK008B070P1&cluster=6100.f. Contact :
              Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DK008B070P1.
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                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT    244 a 265 c 282 g 199 t
ORIGIN
Query Match    51.2%; Score 915.8; DB 9; Length 994;
Best Local Similarity 98.4%; Pred. No. 1.1e-126;
Matches 934; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

QY 35 CCGGAGAGAGTCTCTGACGCCGAGTCCGAGGATAAAGCTTGGGGTTCATCTCTCTCC 94
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QY 515 TGGCAATGGGGCCCTTGTGAGCATCTGTACAAAGATATGGAGAGATGCTCTGGACAAG 574
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RESULT 12
AL514330
LOCUS
DEFINITION
AL514330 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
AL514330
ACCESSION
VERSION
AL514330.2 GI:30464215
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12777824.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB011ZH02RPI&cluster=6100.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB011ZH02RPI.
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                with a NotI-oligo(dT) primer. Five prime end enriched,

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double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 259 a 288 c 309 g 251 t 64 others

Query Match 51.1%; Score 915; DB 9; Length 1201;

Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;

Matches 944; Conservative 29; Mismatches 21; Indels 3; Gaps 3;

108 CAGTCTCAGGCTTCCCAATTCAGAGGAGCTGGCGCGGACGCTGCTATGAGACAT 167

80 CCGTCTCAGGCTTCCCAATTCAGAGGAGCTGGCGCGGACGCTGCTATGAGACAT 139

168 TTTCACTCAGTCCGGGAGGAGCAACGAGTGGCGGCTTGGCGGCTGGGACACAGCGA 227

140 TTTCACTCAGTCCGGGAGGAGCAACGAGTGGCGGCTTGGCGGCTGGGACACAGCGA 199

228 GAACGAGCTCAACAGAGGGGAGCATCATGGCTTCCCTTGCAGTGGGCTGGCGGAGA 287

200 GAACGAGCTCAACAGAGGGGAGCATCATGGCTTCCCTTGCAGTGGGCTGGCGGAGA 259

288 GGGCGGCTCTGCTGTGGTGAAGTGTGATCATGCGGGGGGACGAGTCAATGTATGAA 347

260 GGGCGGCTCTGCTGTGGTGAAGTGTGATCATGCGGGGGGACGAGTCAATGTATGAA 319

348 CCGTGGGGATGACACCCCTGCAATCTGGGAGCCGATGAGACCCGCTGATTTATGCA 407

320 CCGTGGGGATGACACCCCTGCAATCTGGGAGCCGATGAGACCCGCTGATTTATGCA 379

408 GAACGATTTGGAGTCAACAGGAGCATCATGAGTGAATGAACAAGGGAATGTGCCCT 467

380 GAACGATTTGGAGTCAACAGGAGCATCATGAGTGAATGAACAAGGGAATGTGCCCT 439

468 GCATGATGCTGTTTGGGGGCAAGATCAATGAGCAGAGGACCTGTGTGCAAAATGGGGC 527

440 GCATGATGCTGTTTGGGGGCAAGATCAATGAGCAGAGGACCTGTGTGCAAAATGGGGC 499

528 CCTGTGAGCATCTGTACAAGTATGAGAGATGCTGTGACAAGGCAAGGACCCCT 587

500 CCTGTGAGCATCTGTGTACAAGTATGAGAGATGCTGTGACAAGGCAAGGACCCCT 559

588 GAGAGAGCTTCTCCGAGAGCGGAGAGAGATGGGCGAGATCTCAACCGTATTTCCATA 647

560 GAGAGAGCTTCTCCGAGAGCGGAGAGAGATGGGCGAGATCTCAACCGTATTTCCATA 619

648 CAAGGACACATTTGGAAGGGGACCAAGGCTGAGGCGGCGGAAATGGAACCTGAACAA 707

620 MAAGGAMAMATTCTGGAAGGGGACCAAGGCTGAGGCGGCGGAAATGGAACCTGAACAA 679

708 ACATCTTGGGATTTGATCTTCAACAGCTTAACCTTCTGACGAAGCTCAACGGAATCACTC 767

680 AMATCTTGGGATTTGATCTTCAACAGCTTAACCTTCTGACGAAGCTCAACGGAATCACTC 739

768 TGGAGAGCTATGGAAGGGCGGCTGGAGAGGCAATGATGTCGTAAGTGTGAGAGT 827

740 TGGAGAGCTATGGAAGGGCGGCTGGAGAGGCAATGATGTCGTAAGTGTGAGAGT 799

828 TCGAGAGCTGAGTACAGGAAGAGCAGGACTTCAATGAGAGTGTCCCGGCTCAGGAT 887

800 TCGAGAGCTGAGTACAGGAAGAGCAGGACTTCAATGAGAGTGTCCCGGCTCAGGAT 859

888 TTTTCTCGATCCAATGTGCTCCAGTGTAGTGTGCTGCGGAGTCTCAACTGCTCTCA 947

860 TTTTCTCGATCCAATGTGCTCCAGTGTAGTGTGCTGCGGAGTCTCAACTGCTCTCA 919

948 TCTACTCTCATCACACTGGATGCGTATGATCCCTTACATGACTACTACATGAAG 1007

920 TCTACTCTCATCACACTGGATGCGTATGATCCCTTACATGACTACTACATGAAG 979

1008 CACCAATTTGCTGTGAGCAGAGCAGGCTGTGAAGTTTGTGTCATGAGCAGAGGGG 1067

980 C-MCAATTTGCTGTGAGCAGAGCAGGCTGTGAAGTTTGTGTCATGAGCAGAGGGG 1037

Qy 1068 CATGACCTTCTACACACTAGAGCCCTCATCCCA 1104

Db 1038 -MTGGCCTTCYMAAAMAAAAAACCCYHTCCCCMA 1073

RESULT 13

EX363152 1201 bp mRNA linear EST 05-MAY-2003

LOCUS

DEFINITION BX363152 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens

ACCESSION BX363152

VERSION BX363152

KEYWORDS 5-PRIME, mRNA sequence.

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f For more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK009CB08QPlcluster=6100.f. Contact: Feng Liang Email: fliang@life.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Parady Avenue Genoscope sequence ID: CS0DK009CB08QPl.

FEATURES

source

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DK009YD15"

/cell_type="HELA CELLS COT 25-NORMALIZED"

/cell_line="HELA"

/note="First strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 286 a 305 c 318 g 244 t 48 others

ORIGIN

Query Match 51.0%; Score 912.6; DB 13; Length 1201;

Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;

Matches 984; Conservative 13; Mismatches 37; Indels 7; Gaps 5;

Qy 46 TCCGAGACCCGAGTCCCGAGGATTAAGCTTGGGCTTCATCCCTCCGATCACTC 105

Db 21 TCCGAGACCCGAGTCCCGAGGATTAAGCTTGGGCTTCATCCCTCCGATCACTC 80

Qy 106 CACAGTCTCAGGCTTCCCAATCCAGAGGAGCTGGGCGCGGAGCGTGTATGAGAGC 165

Db 81 CACAGTCTCAGGCTTCCCAATCCAGAGGAGCTGGGCGCGGAGCGTGTATGAGAGC 140

Qy 166 ATTTCCTCAGTCCGGGAGGAGCAAGCAGTCCCGTGGCTGTGCTGGAACAACG 225

Db 141 ATTTCCTCAGTCCGGGAGGAGCAAGCAGTCCCGTGGCTGTGCTGGAACAACG 200

Qy 226 GAGAGACCTCAACAGAGGGGAGCATGAGGCTTCCCGCTTGAACGAGGCTGCGGA 285

Db 201 GAGAGACCTCAACAGAGGGGAGCATGAGGCTTCCCGCTTGAACGAGGCTGCGGA 260

Qy 286 GAGGCGGCTCTGCTGTGTGATGATTTGATCAATGCGGGGGGACGAGATCAATGATG 345

Db 261 GAGGCGGCTCTGCTGTGTGATGATTTGATCAATGCGGGGGGACGAGATCAATGATG 320

QY 346 AACCTGGGATGACACCCCTCTGCATCTGGCAGCAGTCATGGACACCGTGTATTTGA 405
 Db |||||
 QY 321 AACCTGGGATGACACCCCTCTGCATCTGGCAGCAGTCATGGACACCGTGTATTTGA 380
 Db |||||
 QY 406 CAGAAGCTATTGACGTACAGGACAGACATCAATGACGTGAATGAACAGGGAATGTGCC 465
 Db |||||
 QY 381 CAGAAGCTATTGACGTACAGGACAGACATCAATGACGTGAATGAACAGGGAATGTGCC 440
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 QY 466 CTGCACTATGCTGTTTTTGGGGCCAAAGATCAAGTGGCAGAGGACCTGGTGGCAATGGG 525
 Db |||||
 QY 441 CTGCACTATGCTGTTTTTGGGGCCAAAGATCAAGTGGCAGAGGACCTGGTGGCAATGGG 500
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 QY 886 ATTTTCTCGCATCCAAATGTCTCCAGTGTCTAGGTGCTGCGAGCTTCCACCTGCTCT 945
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 QY 918 CATCTTATCTCATCACACAKGGATGCGTATGGATCCCTT-CAATGTACTAMTTGAA 976
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 QY 1006 GGCACCAATTTCTGCTGGACAGCAGGCTGTGAAGTTTGTCTTTGGACATGSCAAGG 1065
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 QY 977 GGACCAAAATTTCTCKGACAAAACCAAGGYDT---TAATTTTCTTGTGAMWKAAGG 1033
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 QY 1034 GGATVGGCTTCTACAAAYAA 1054
 Db |||||

RESULT 14
 BX340064/c
 LOCUS
 DEFINITION BX340064 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1081YL01 3-PRIME, mRNA sequence.
 ACCESSION BX340064
 VERSION BX340064.1 GI:30333861
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6100.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1081CF01NP1&cluster=6100.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1081CF01NP1.

FEATURES source

1. 1201
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 264 a 281 c 305 g 305 t 46 others
 ORIGIN
 Query Match 51.0%; Score 911.6; DB 13; Length 1201;
 Best Local Similarity 95.8%; Pred No. 4.2e-128;
 Matches 976; Conservative 12; Mismatches 23; Indels 8; Gaps 5;
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 QY 1014 TTACTTCAACAGCTTA-CTCTACAAAGCTCAACAAAAATACTCTGRAGAGCTATG 957
 Db |||||
 QY 780 GAAGGGCGCTGGCGCAATGACATTTCTGTGAGGTGCTGAAGGTTCGAGACTGGAG 839
 Db |||||
 QY 956 GAA-GGCCGCTGGCAGGCAATTAACATTTCTGTGAAGGTGCTGAAGGTTCGADATGGAG 898
 Db |||||
 QY 840 TACAAGGAAGACAGGAGCTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCC 899
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 QY 897 AACAGGAAGACAGGAGCTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCC 838
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 QY 900 AAATGTGTCTCCAGTGTAGTGTGCTGCAAGTCTCCACCTGCTCTCTCTCTCTCTCTCT 959
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 QY 717 CQTGACACAGCAGGCTGTGAAGTTTGTGTTGACATGGCAAGGCGATGGCTTCTCTCA 658
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 QY 417 GGAGGTACCTTTGCTGACCTCTCAATATGGAGATTGGAATGAGGTGGCATTTGGAAGG 358
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 Db |||||

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Db      357  --ATGGGCTACATCCACAGGATTTCCCTCATGTGTAGCTCATGAAGATCTG 300
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Db      299  CATGATTAAGACCTCTGCAAGCAGCCAAATTTTACATGATTTGCTTATCTTGAGAA 240
Qy      1500 GATCAGAGCAAGATGAGACTGGAAGGCTCTGCTGGAAGCTCAGAGGCTGGGGCATGG 1559
Db      239  GATCAGAGCAAGATGAGACTGGAAGGCTCTGCTGGAAGCTCAGAGGCTGGGGCATGG 180
Qy      1560 TTGGGGGAATGACCTCTCCCAAGCAGGAGGCTGTTGCTCTCCCGCTCCAGTCA 1619
Db      179  TTGGGGGAATGACCTCTCCCAAGCAGGAGGCTGTTGCTCTCCCGCTCCAGTCA 120
Qy      1620 TGTGACTACCCAGCC-TGGGGTCCATCCCTTCCCACTCACTGTG--CGCAA 1676
Db      119  TGTGACTACCCAGCCAGGAGGCTGTTGCTCTCCCGCTCCAGTCACTGTGGCCCAA 60
Qy      1677 GAGGGGCGGGCTCAGAGCTTTGTCTGCACTGATGCTGCCAAGATGGAGGAT 1735
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RESULT 15
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DEFINITION BX340065 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
          clone CS0D1081YL01 5-PRIME, mRNA sequence.
ACCESSION BX340065
VERSION  BX340065
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 Evry cedex - France
          Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Invitrogen. This sequence belongs to sequence cluster 6100.f For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0D1081CP01QPLcluster=6100.f. Contact :
          Feng Liang Email : fliang@lifetech.com URL : Corporation 1600
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              digested with NotI and cloned into the NotI and EcoRV
              sites of the pCMVSPORT 6 vector. Library was normalized."

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BASE COUNT 288 a 295 c 315 g 252 t
ORIGIN

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Query Match 50.9%; Score 909.8; DB 13; Length 1201;
Best Local Similarity 98.3%; Pred. No. 7.9e-128;
Matches 923; Conservative 6; Mismatches 8; Indels 2; Gaps 1;
Qy 25 CGGAGTCCCCCGAAGATCTCGAGCCGAGTCCCGAGATTAAGCTTGGGTTCA 84
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Db      125  TCCTTCCTTCCCTGGATCATCTCCACAGTCTCTAGGCTTCCCAATTCAGGGGATCTCGGGC 184
Qy      145  CGGAGCTGCTATGAGAGCATTTTCACTCAGTGGCCGGAGGCAACGAGTGGCCGCTT 204
Db      185  CGGAGCTGCTATGAGAGCATTTTCACTCAGTGGCCGGAGGCAACGAGTGGCCGCTT 244
Qy      205  CGCCTGTGCTGGAACAACGAGAGAACGACTCAACGAGGGGAGCATCATGCTTCTCC 264
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Qy      265  CCCTTTCAGTGGGCTGCGGAGAGGCGCTCTGCTGTGGTTGAGATTTGATCATGGCG 324
Db      305  CCCTTTCAGTGGGCTGCGGAGAGGCGCTCTGCTGTGGTTGAGATTTGATCATGGCG 364
Qy      325  GGGGACGGATCAATGTATGAACCGTGGGGATGACACCCCTGCACTGGCAGCCAGT 384
Db      365  GGGGACGGATCAATGTATGAACCGTGGGGATGACACCCCTGCACTGGCAGCCAGT 424
Qy      385  CATGACACCGTGAATATTGTAAGAGGATTTGAGATCAAGGACATCATATGACAGTG 444
Db      425  CATGACACCGTGAATATTGTAAGAGGATTTGAGATCAAGGACATCATATGACAGTG 484
Qy      445  AATGACACGGGAAATGTCCTCTGCACTATCTCTGTTTGGGGCAAGATCAAGTGGCA 504
Db      485  AATGACACGGGAAATGTCCTCTGCACTATCTCTGTTTGGGGCAAGATCAAGTGGCA 544
Qy      505  GAGGACCGTGGGAAATGAGGCGCTTGTGCACTCTGTAACAGTATGAGAGATGGCT 564
Db      545  GAGGACCGTGGGAAATGAGGCGCTTGTGCACTCTGTAACAGTATGAGAGATGGCT 604
Qy      565  GTGACAAAGCCAGAGGACCCCTGAGAGGCTTCCGAGACGGGCGAGAGATGGGC 624
Db      605  GTGACAAAGCCAGAGGACCCCTGAGAGGCTTCCGAGAGCGGGCGAGAGATGGGC 664
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Qy      685  CCCCAGATGGAACCCGTAACAAACACTGTGGCACTTCAACAGCTTAACCTCTG 744
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Db      905  GAAAGGTGCTCCCGGCTCAGAGATTTTCCGATCCAAATGCTGCCAGCTCTAGGTCC 964
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Job time : 2624 secs

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